xenopus lae xenopus lae

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29W7R9 2910C0 296QB3 29UML6 Q8N6U4

Q7TMS0 Q910B9

Q62032 Q80X38 Q80VY3

062033

Q62031

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PRELIMINARY;
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                                           6; Search time 21.0943 Seconds (without alignments) 3126.121 Million cell updates/sec
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1 GPPGEPGPTGLPGPPGERGG.......GEQGVPGDLGAPGPSGPAGG 209
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       GenCore version 5.1.6 (c) 1993 - 2004 Compugen Ltd.
                                                                                                                             Total number of hits satisfying chosen parameters:
                                                                                                               1017041 seqs, 315518202 residues
                                             September 24, 2004, 11:06:56;
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Listing first 45 summaries
                                protein search, using sw model
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sp_virus:*
sp_vertebrate:*
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Q8awll brachydanio Q90yj0 brachydanio Q8uuj4 oncorhynchu Q8uuj3 oncorhynchu Q80lm5 xenopus lae

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Q8AW11

OBBLW4 Q7TT32 Q8CGA5 Q15177 Q7Z5S6

Q8K173 Q8BKY2

QBCFM4

061431

ALIGNMENTS

[3]
SEQUENCE FROM N.A.
MEDLINE=89025644; PubMed=3178743;
Tronp G., Kuivaniemi H., Stacey A., Shikata H., Baldwin C.T.,
Jaenisch R., Prockop D.J.;
"Structure of a full-length cDNA clone for the prepro alpha 1(I) chain
of human type I procolagen.";
Biochem. J. 253:919-922(1988). [1]
SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
MEDLINE=85130970; PubMed=2857713;
Chu M.L., de Wet W., Bernard M., Ramirez F.;
Chu M.L., de Wet W., Bernard M., Ramirez F.;
"Fine structural analysis of the human pro-alpha 1 (1) collagen gene.
"Fine structural analysis of the human pro-alpha 1 (1) collagen gene.
Promoter structure, AluI repeats, and polymorphic transcripts.";
J. Biol. Chem. 260:2315-2320(1985). MEDLINE-88329734; PubMed=2843432; D'Alessio M., Barnard M., Pretorius P.J., de Wet W., Ramirez F.; D'Alessio M., Bernard M., Pretorius P.J., de Wet W., Ramirez F.; Complete nucleotide sequence of the region encompassing the first twenty-five exons of the human pro alpha 1(1) collagen gene."; Gene 67:105-115(1988). Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi, Mammalia; Butheria; Primates, Catarrhini; Hominidae, Homo. NCBI_TaxID=9606; Created) Last sequence update) Last annotation update) PRT; 1461 AA SEQUENCE FROM N.A. MEDLINE=91138770; PubMed=1995349; Maatta A., Bornstein P., Penttinen R.P.; 076045; 01-NOV-1998 (TrEMBLrel. 08, 01-NOV-1999 (TrEMBLrel. 12, 01-OCT-2003 (TrEMBLrel. 25, Pro alpha 1(I) collagen.

Q83079 rattus norv Q81019 mus musculu Q9y1b4 cynops pyrr Q95251 rana catesb Q91025 xenopus lae Q91091 xenopus lae Q28396 equus cabal Q77753 canis famil Q7727 gallus gall Q10037 gallus gall Q10037 gallus gall Q1047 homo sapien Q1717 xenopus lae Q27117 xenopus lae

Q8N473 Q63079 Q810J9 Q9XIB4 Q93251 Q802B5 Q91B91 Q28396

1461 1464 1453 1453 1453 1445 1444 1418 1418 1160 1160 1160 11484 1486

11149 11122 11116 989 981 941 860 860 885 859 859 859 859 850 850 850 850

Q14046 Q7T2Z7 Q90W37

Q14047 Q91717 Q72TI6

076045 homo sapien homo sapien

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Hypothetical
Homo sapiens
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KOTKAC J.M., Barley J.J., Nuytinck L., DePaepe A., Prockop D.J.,
Slanitted (MAY-1999) to the EMBL/GenBank/DDBJ databases.

SUBMIL; AF017178; AA994054.2; --
GO; GO:0005581; C:collagen; IEA.
GO; GO:0005201; F:extracellular matrix structural constituent; IEA.
InterPro; IPR008161; Clg_helix.
InterPro; IPR008161; Clg_helix.
InterPro; IPR008181; Fibrinogen.
InterPro; IPR008181; Fibrinogen.
InterPro; IPR001885; Fib_collagen.
InterPro; IPR001885; Fib_collagen_C.
InterPro; IPR001885; Fib_collagen_C.
InterPro; IPR001087; VWF_C.
                                                                                                                                                                                 MEDIANCE 99107942; PubMed=9443882; Körkko J., Ala-Kokko L., De Paepe A., Nuytinck L., Earley J., Prockop D.J.; Prockop D.J.; Rahalysis of the COLIA1 and COLIA2 genes by PCR amplification and scanning by conformation-sensitive gel electrophoresis identifies (COLIA1 untations in 15 patients with osteogenesis imperfecta type identification of common sequences of null-allele mutations."; Am. J. Hum. Genet. 62:98-110(1998).
    region of the
                                                      SEQUENCE FROM N.A.
MEDILINE=59157916; PubMed=1787829;
MEDILINE=59157916; PubMed=1787829;
Westerhausen A., Constantinou C.D., Pack M., Peng M.Z., Hanning Olsen A.S., Prockop D.J.;
"Completion of the last half of the structure of the human gene the Pro alpha 1 (1) chain of type I procollagen (COLIAI).";
Matrix 11:375-379 (1991).
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 "Highly conserved sequences in the 3'-untranslated COLIA1 gene bind cell-specific nuclear proteins."; FEBS Lett. 279:9-13(1991).
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Matches 206; Conservative
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49 GPKGSPGEAGRPGEAGLPGAKGLTGSPGSPGPDGKTGPPGPAGQDGRPGPPGPPGARGQA 108
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                                                                                                                                                                          Strausberg R.;
Strausberg R.;
Submitted (AUG-2002) to the EMBL/GenBank/DDBJ databases.

Submitted (AUG-2002) to the EMBL/GenBank/DDBJ databases.

BMSL; BC036531; AAH6531.1;
R GO; GO:0005201; F:collagen; IEA.

GO; GO:0005201; F:extracellular matrix structural constituent; IEA.

R GO; GO:0005201; F:extracellular matrix structural constituent; IEA.

R GO; GO:0005201; F:extracellular matrix structural constituent; IEA.

R InterPro; IPR00181; Clagen.C.

R InterPro; IPR00181; Fibrinogen.C.

R InterPro; IPR001008; Fibrinogen.C.

R FRODOM; PF001907; VWF.C.

R ProDom; PF01391; Collagen; 18.

R PRODOM; PB000007; Glg.helix; 2.

R PRODOM; PB000007; Glg.helix; 2.

R SMART; SM00038; COLFI; 1.
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Brandsten C., Lundmark C., Christersson C., Hammarstrom L., Wurtz T.;
"Expression of Collagen alphal(I) mRNA variants during Tooth and Bone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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01-NOV-1998 (TrEMBLrel. 06, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Collagen alphal (Fragment).
Eattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                   Eukaryofa, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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PROSITE; PS01084; WWPC_2; 1.
Hypothetical protein; Collagen.
SEQUENCE 1464 AA; 139011 MW; BOS81F8D1C89DDE8 CRC64;
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93.6%; Pred. No. 8.1e-72;
ive 0; Mismatches 2;
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STRAIN=Sprague-Dawley, TISSUE=Tooth;
Wurtz T.;
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Matches 206; Conservative
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(Human)
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TISSUE=Brain;
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STRAINSFURNING TISSUE=COLON;
STRAINSFURNING TISSUE=COLON;
REMBL; BCOSCO14; AAHSOO14.1; -.
RED; BCOSCO15; FCCOLONG TIEA.
RED; PRO0015581; CCOLONG TIEA.
RED; PRO001861; FIDINGOGON.
RICEPPO; IPRO001861; FIDINGOGON.
RICEPPO; IPRO0107; VWF.C.
RED; PRO0107; VWF.C.
RED; PRO0107; FIDINGOGN.
RED; PRO0107; FIDINGOGN.
RED; PRO0107; FIDINGOGN.
RED; PRO0107; VWF.C.
RED; PROSITE; PSSO184; VWF.C.
RED; PSSO184; VWF.C.
R
           EMBL, 278279; CABGGG33.1; -.

R GO, GO.005581; C.collagen; IEA.

GO, GO.005581; C.collagen; IEA.

GO, GO.005581; C.collagen; IEA.

GO, GO.005201; F:extracellular matrix structural constituent; IEA.

R InterPro; IPR008160; Collagen.

R InterPro; IPR008181; Fibrinogen.C.

R InterPro; IPR001007; VWF_C.

R InterPro; IPR001007; VWF_C.

R Ffam; PF01139; Collagen; I.

R Frobom; PD0100007; Clg helix; 3.

R Probom; PD0100007; Clg helix; 3.

R SWART; SM00138; COLFI; 1.

R SWART; SM00138; COLFI; 1.

R ROSITE; PS01208; VWFC_1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q81019;
01-JUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 25, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Hypothetical protein.
Mus musculus (Mouse).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match

94.8%; Score 1122; DB 11; Length 1453;
Best Local Similarity 91.4%; Pred. No. 5.9e-70;
Matches 201; Conservative 2; Mismatches 5; Indels 12;
                                                                                                                                                                                                                                                                                                                                                                         Collagen.
NON TER 1 1 SEQUENCE 1453 AA; 137887 MW; E6896BDC19A4AlD8 CRC64;
Submitted (FEB-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GSPGFQGLPGPAGPPGEAGKPGEQGVPGDLGAPGPSGPAG 208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GSPGFOGLPGPAGPPGEAGKPGEOGVPGDLGAPGPSGARG 666
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT; 1453 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     49 GPKGSPGEAGRPGEAGLPGAKGLTGSPGSPGPDGKTGPPGPAGQDGRPGPPGPPGARGQA 108
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TISSUE REGENERATE forelimbs;

XX MEDINES 95407244; PubMed=1044166;

XX MEDINES 95407244; PubMed=1044166;

Asahina K., Obara M., Vashizato K.;

Asahina K., Obara M., Vashizato M.;

BML; Asubisation of genes of type I and type II collagen in the formation and development of the blasten and development of the formation and development of the plant matrix structural constituent; IEA.

BML; Asholsof M. Collagen.

BR Fram; PRO1410; Colle M. M.F.

BR Fram; PRO1410; Colle M. M. Parena M. Barena M. Barena
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01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Alpha 1 type I collagen.
Cynops.pyrthogaster (Japanese common newt).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Caudata; Salamandroidea; Salamandridae; Cynops.
NCBL TaxID-8330;
                                                                                                                                                                                                                12;
                                                                                                                      Length 1453;
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80.5%; Pred. No. 9.5e-61;
iive 7; Mismatches 24; Indels 12.
                                                                                                                                                                                                                Indels
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Hypothetical protein.
SEQUENCE 1453 AA; 138032 NW; 0B7F06BBB9AlD5EA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               169 GSPGFOGLPGPAGPPGEAGKPGEOGVPGDLGAPGPSGPAG 208
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                                                                                                                 Query Match
94.3%; Score 1116; DB 11;
Best Local Similarity 90.5%; Pred. No. 1.5e-69;
Matches 199; Conservative 4; Mismatches 5;
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Q9YIB4;
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NCBI_TaxID=8355;
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MEDLINE=99294154; PubMed=10367734;
Asahina K., Utoh R., Obata M., Yoshizato K.;
Asahina K., Utoh R., Obata M., Yoshizato K.;
Cell-type specific and thyroid hormone-dependent expression of genes amphibianmetamorphosis: ";
Matrix Biol. 18:89-103(1999).

EMBL; AB015440; BAA29028.1; ".
CG; GG:0005581; C:collagen; IEA.
GG; GG:0005581; C:collagen; IEA.
InterPro; IPR008161; Clg_helix.
InterPro; IPR008161; Clg_helix.
InterPro; IPR008161; Clg_helix.
InterPro; IPR008161; Clg_helix.
InterPro; IPR000181; Fibrinogen_C.
InterPro; IPR00181; Fibrinogen_C.
InterPro; IPR00181; Collagen; 18.
ProDom; PP001007; VWF_C.
Refm; PF01140; Coller; 1.
Refm; PF01140; Coller; 1.
Refm; PF01189; Collagen; 18.
Refm; PF01089; Coller; 1.
Refm; PF01089; COLDE; 1.
Refm; PF01089; COLDE; 1.
Refm; PF01080; COLDE; 1.
Refm; PF01081; Collagen; 18.
Refm; Refm; PF01081; Collegen; 18.
Refm; PF01081; Collegen; 18.
Refm; PF01081; PF01081; Collegen; 18.
Refm; PF01081; PF01081; Collegen; 18.
Refm; PF01081; Fib_collagen_C; 1.
Refm; PF01081; Fib_collagen_C; 1.
Refm; Refm; PF01181; Collegen; 18.
Refm; Refm; PF01181; Collegen; 18.
Refm; 
                                                 GVMGFPGPKGAAGEPGKAGERGVPGPPGAVGPAGKDGEAGAQGPPGPAGPAGERGEQGPA 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         146 GPPGEEGKRGSRGEPGPPGPAGERGAPGSRGFPGADGAGGPKGPPGERGPVGSAGPK 505
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GFPGPKGAAGEPGKAGERGVPGPPGAVGPAGKDGEAGAQGPPGPAGPAGERGEQGPAGSP 171
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Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.
NCBI_TaxID=8400;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 82.9%; Score 981; DB 13; Length 1445; Best Local Similarity 82.0%; Pred. No. 3.4e-60; Matches 178; Conservative 5; Mismatches 22; Indels 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1445 AA; 137252 MW; F59BB550C9873F04 CRC64;
                                                                                                            208
                                                                                                                                      624 GSPGFQGLPGSPGPAGEAGKPGEQGAPGDAGGPGPSGPRG 663
                                                                                                                                                                                                                                                                                                        01-NOV-1998 (TrEMBLrel. 08, Created)
01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
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Rana catesbeiana (Bull frog)
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                                                                                                                                                                                                                                                                PRELIMINARY;
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SEQUENCE
                     109
                                                                                                       169
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PRT; 1449 AA.

PRELIMINARY;

RESULT 7 Q802B5 ID Q802B5

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563
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KIEAIN S., Strausberg R.;

KIEAIN BC048829; AAH49829.1; -..

KIEACO GO:0005581; C:collagen; IEA.

GO; GO:000501; F:carracellular matrix structural constituent; IEA.

INTERPO: IPRO00885; Fib_collagen.

R InterPro; IPRO00885; Fib_collagen.

R InterPro; IPRO01007; VWF_C.

R Pfam; PF01410; Collagen; 18.

R ProDon; P0002078; Fib_collagen_C; 1.

K PRODON; P0002078; Fib_collagen_C; 1.

K RAMART; SW00214; VWC. 1.
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Goto T., Katada T., Kinoshita T., Kubota H.Y.;

"Expression and characterization of Xenopus type I collagen alpha 1
(CDLJA1) adving embryonic development.";

Submitted (NOV-1999) to the EMBL/Genbank/DDBJ databases.

EMBL; AB034701; BAA94972.1; -.
                                                                               Hypothetical protein.
Xenopus laevis (African clawed frog).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Amphibia, Batrachia, Anura, Mesobatrachia, Pipoldea, Pipidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Xenopus laevis (African clawed frog).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Amphibia, Batrachia, Anura, Mesobatrachia, Pipoidea, Pipidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       81.3%; Score 962.5; JB 13; Length 1449; 79.5%; Pred. No. 6.5e-59; ive 8; Mismatches 22; Indels 15;
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01-JUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
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01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-UN-2003 (TrEMBLrel. 24, Last annotation update)
Type I collagen alpha 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PROSITE; PS01208; VWFC_1; 1.
PROSITE; PS50184; VWFC_2; 1.
HYDOLHetical protein.
SEQUENCE 1449 AA; 137464
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches 175; Conservative
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NCBL_TaxID=8355;
                                                                                                                                                                                                          Xenopodinae; Xenopus.
                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
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423 GARGEPGGAGPVGPPGERGAPGNRGFPGQDGLAGPKGAPGERGPSGLAGPKGANGDPGRP 482
                                                                                                                                                                                                                                                                                                              61 GEAGLPGAKGLTGSPGSPGPDGKTGPPGPAGQDGRPGPPGARGQAGVMGFPGPKGAA 120
                                                                                                                                                                                                                                                                                                                                                     121 GEPGKAGERGVPGPPGAVGPAGKDGEAGAQGPPGPAGPAGERGEQGPAGSPGFQGLPGPA 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              543 GEPGKAGEKGLPGAPGLRGLPGKDGETGAAGPPGPAGPAGERGEQGAPGPSGFQGLPGPP 602
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MEDLINE=88340220; PubMed=8676231;
Du F., Acland G.M., Ray J.;
"Differential splicing of type II procollagen mRNA in canine retina.";
Anim. Biotechnol. 9:15-20(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL: AF02169; AAC62178.2;

R GO; GO: 0005581; C: collagen; IEA.

GO; GO: 0005581; C: collagen; IEA.

GO; GO: 0005581; C: collagen; IEA.

R InterPro; IPR008160; Collagen.

R InterPro; IPR00885; Fib collagen.

R InterPro; IPR0010885; Fib collagen.

R Pfam; PF01410; COLFF; 1.

R Pfam; PF01410; COLFF; 1.

R Pfam; PF000007; Clg helix; 4.

R ProDom; P000007; Clg helix; 4.

R ProDom; P000017; Clg helix; 4.

R SMART; SM00218; VWC; 1.

R SMART; SM00218; VWC; 1.

R PROSITE; PS50184; VWFC_1; 1.
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Mammalia, Eutheria, Carnivora, Fissipedia, Canidae, Canis.
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MEDLINE-20480698; PubMed-11024291;
Du F., Acland G.M., Ray J.;
"Cloning and expression of type II collagen mRNA: evaluation as candidate for canine oculo-skeletal dysplasia.";
Gene 255:307-316(2000).
                                                                                                                                  .
0
                                                                      Length 1418;
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                                                                                                                               44; Indels
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            1418 AA; 134343 MW; 115FCD19EB8696A3 CRC64;
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Last annotation update)
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                                                                      12.6%; Score 860; DB 6; larity 74.0%; Pred. No. 7.9e-52; Conservative 10; Mismatches 44
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       181 GPPGEAGKPGEQGVPGDLGAPGPSGPAG 208
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
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Canis familiaris (Doc
                                                            Query Match
Best Local Similarity
Matches 154; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         110 VMGPPGPKGAAGEPGKAGERGVPGPPGAVGPAGKDGEAGAQGPPGPAGPAGERGEQGPAG 169
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      444 GPPGPSGEBGKRGSRGEPPAGPPGPAGERGGPGSRGFPGSDGASGPKGAPGERGPVGPAG 503
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GPPGEPG------PTGLPGPPGERGGPGSRGFPGADGVAGPKGPAGERGSPGPAG 49
RGO; GO:0005581; C:collagen; IEA.
RGO; GO:0005201; F:extracellular matrix structural constituent; IEA.
RINGERFO; IFR003861; C1g helix.
RINGERFO; IFR003861; C2lagen.
RINGERFO; IFR001007; COLFID.
RINGERFO; IFR001007; VWF_C.
RINGERFO; IFR001007; VWF_C.
REPROSE PERONOSS; Fib_collagen_C.
REPROSE PERONOSS; VWC; 1.
REPROSE PERONOSS; VWC; 1.
REPROSE PERONOSS; COLFI; 1.
REPROSE RE
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-UNY-2003 (TrEMBLrel. 24, Last annotation update)
Type II collagen.
Type II collagen.
Eduus caballus (Horse).
Eukaryota, Metacoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Perissodactyla, Equidae, Equus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 941; DB 13; Length 1447;
Pred. No. 2e-57;
8; Mismatches 25; Indels 14;
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Richardson D.W., Dodge G.R.;
Submitted (JUN-1996) to the EMBL/GenBank/DDBJ databases.
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MacLeod J.W., Fubini S.L., Gu D.N., Tetreault J.W., Tod
Submitted (DEC-1997) to the EMBL/GenBank/DDBJ databases
EMBL; U62528; AABO5773.1; -.
EMBL; AF040638; AAB96768.1; -.
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PROSITE; PS50184; VWFC_2; 1.
SCOLBGEN.
SEQUENCE 1447 AA; 137446 I
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Best Local Similarity 78.5
Matches 172, Conservative
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01-OCT-2003 (TrEMBLrel. 25, Created)
01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
02-02-02-02-02-03-03-03-03-03-03-03-03-03
                                                                                                                                 Gallus gallus (Chicken)
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SEQUENCE
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  492 GARGEPGGAGPVGPPGERGAPGNRGFPGQDGLAGPKGAPGERGPSGLAGPKGANGDPGRP 551
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"Structure of cDNA clones coding for human type II procollagen. The
alpha 1(II) chain is more similar to the alpha 1(I) chain than two
other alpha chains of fibrillar collagens.";
Biochem. J. 262:521-528(1989).
BMILL, XIG711; CAA34683.1;
InterPro; IPRO08161; Clg hellx.
InterPro; IPRO08161; Clg hellx.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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113 > 1160 COLLAGEN.
1160 1160 MW; A7F0523B856C8639 CRC64;
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
COL2A1 protein precursor (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT; 1160 AA.
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MEDLINE=90026318; PubMed=2803268;
Smit
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ProDom; PD0000007; Clg_helix; 4.
Collagen; Signal. 23 PO:
SIGNAL 1
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SEQUENCE
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PRT; 1269 AA

PRELIMINARY;

Q7T227, Q7T227;

RESULT 12 Q7T2Z7

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         121 GEPGKAGERGVPGPPGAVGPAGKDGEAGAQGPPGPAGPAGERGEQGPAGSPGFQGLPGPA 180
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A Caixia X., Yongzhi X., Siqi G., Yiying S.;
Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
R Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
R GO; GO:0005201; F:extracellular matrix structural constituent; IEA.
R InterPro; IPRO0816; Collagen.
R InterPro; IPRO0886; Fibrinogen.C.
InterPro; IPRO0886; Fibrinogen.C.
R Pfam; PF01410; COLFF; 1.
R Pfam; PF01410; COLFF; 1.
R Pfam; PF01410; COLFF; 1.
R PF00m; PD000007; CIg_helix; 6.
R ProDom; PD000007; CIg_helix; 6.
R PRODM; PR00189; COLFF; 1.
Collagen; Signal.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Archosauria, Aves, Neognathae, Galliformes, Phasianidae, Phasianinae,
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Caixia X., Yongzhi X., Siqi G., Yuying S.;
"Gallus gallus alpha I type IIA collagen precursor (CCL2A1).";
Submitted (JUN-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; AF452711; AA033039.2; -.
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1269 AA; 120116 MW; 446EF91BEBE8BF6A CRC64;
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
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Peltonen L
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                                                                                                                                                                           425 GARGEPGAAGPVGPPGERGAPGNRGFPGQDGLAGPKGAPGERGPAGLAGPKGATGDPGRP 484
                                                                         1 GPPGEPGPTGLPGPPGERGGPGSRGFPGADGVAGPKGPAGERGSPGPAGPKGSPGEAGRP 60
                                                     Gaps
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Ryan M.C., Sieraski M., Sandell L.J.;
"The human type II procollagen gene: identification of an additional protein-coding domain and location of potential regulatory sequences in the promoter and first intron.";
Genomics 8:41-48(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Baldwin C.T., Reginato A.M., Smith C., Jimenez S.A., Prockop D.J., "Structure of cDNA clones coding for human type II procollagen. The alpha 1(II) chain is more similar to the alpha 1(I) chain than two other alpha chains of fibrillar collagens.", Biochem. J. 262:521-528(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                          TISSUE=Blood;
MEDINE=BB190534; PubMed=3857598;
Cheah K.S., Stoker N.G., Griffin J.R., Grosveld F.G., Solomon E.;
Identification and characterization of the human type II collagen
                                                                                                                                                                                                                                                                                                                                                                      Craniata, Vertebrata, Buteleostomi,
Catarrhini, Hominidae, Homo.
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                               Length 1420;
                                                     Indels
25 POTENTIAL.
134999 MW; 88D9AAB17F214FF5 CRC64;
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Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    gene (COL2A1).",
Proc. Natl. Acad. Sci. U.S.A. 82:2555-2559(1985).
                                DB 13;
                            72.6%; Score 859; DB 13; 73.6%; Pred. No. 9.3e-52; ive 11; Mismatches 44
                                                                                                                                                                                                                                                                                  PRT; 1487 AA
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Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           gene.";
FEBS Lett. 250:171-174(1989).
                                                                                                                                                                                                                                                                                                    01-NOV-1996 (TrEMBLrel. 01, 01-NOV-1996 (TrEMBLrel. 01, 01-JUN-2003 (TrEMBLrel. 24, Alpha-1 type II collagen.
                                          Best Local Similarity 73.6
Matches 153; Conservative
                                                                                                                                                                                                                                                                                  PRELIMINARY;
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         1420 AA;
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SEQUENCE FROM N.A.
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SIGNAL
SEQUENCE
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Q14047
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=97104294; PubMed=8948452; Ala-Koko L., Kvirikko K.I., Ala-Koko L., Kvist A.P., Metsaranta M., Kivirikko K.I., de Crombrugghe B., Prockop D.J., Vuorio E., Conservation of the sizes of 53 introns and over 100 intronic sequences for the binding of common transcription factors in the human and mouse genes for type II procollagen (COL2A1)."; Biochem. J. 308:0-0(0).

EMBL; L10347; AAC41772.1; -.
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                                                                                                                                                                                                                                                                                                                    "Structural analysis of the regulatory elements of the type-II procollagen gene. Conservation of promoter and first intron sequences between human and mouse.";
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                                                                                    "Genomic organization of the human procollagen alpha 1(II) collagen
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GO; GO:0005201; F:extracellular matrix structural constituent; IEA.
InterPro; IPR008161; Clg.helix.
InterPro; IPR008160; Collagen.
InterPro; IPR00885; Fib.collagen.C.
InterPro; IPR001007; VWF.C.
MEDLINE-91153296; PubMed-1999183;
Huang M.C., Seyer J.M., Thompson J.P., Spinella D.G., Cheah K.S.,
                                                                                                                                                                                                                                                                       Vikkula M., Metsaranta M., Syvanen A.C., Ala-Kokko L., Vuorio E.
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(TrEMBLrel. 01, Last sequence update)
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Pred. No. 9.6e-52;
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Pfan, PF01391; Collagen; 18.
ProDom; PF000007; C1g_helix; 4.
ProDom; PF000007; C1g_helix; 4.
SWART; SM00038; COLFI; 1.
SWART; SM00214; VWC; 1.
                                                                                                                  gene.";
Eur. J. Biochem. 195:593-600(1991)
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Best Local Similarity 74.0'
Matches 154; Conservative
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                                                                                                                                                                                        SEQUENCE FROM N.A. TISSUE=Blood;
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                                                                                                                                                                                                                                                MEDLINE=92344585;
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01-NOV-1996
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01-OCT-2003 (TrEMBLrel. 25, Last annotation update)

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494 GARGEPGAAGPNGPPGERGAPGNRGFPGQDGLAGPKGAPGERGVPGLGGPKGGNGDPGRP 553
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                                                                                                                                                                                                                                   MEDLINE=92011898; PubMed=1918153; Sulursh M., Ramirez F.; Su M.W., Suzuki H.R. Bieker J.J., Solursh M., Ramirez F.; Su M.W., Suzuki H.R. Bieker J.J., Solursh M., Ramirez F.; Expression of two nonallelic type II procollagen genes during Xenopus laevis embryogenesis is characterized by stage-specific production of alternatively spliced transcripts."; J. Cell Biol. 115:565-575(1991).

J. Cell Biol. 115:565-575(1991).

PEMBL, MASS995; AAA49678.1; P.

PIR; A40333; B40333.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       R GO; GO:0005281; C:collagen; IEA.

GO; GO:0005201; F:extracellular matrix structural constituent; IEA.

GO; GO:0005201; F:extracellular matrix structural constituent; IEA.

GO; GO:0005201; F:extracellular matrix structural constituent; IEA.

R InterPro; IPRO08160; Collagen.

R InterPro; IPRO01807; VWF.C.

R Pfam; PPO1391; Collagen.

R Pfam; PPO1391; Collagen; 18.

R ProDom; PD000007; Clg. 11.

R ProDom; PD000007; Clg. 11.

R SMART; SM00214; VWF.C.

R SMART; SM00214; VWF.C. 1.

R PROSITE; PS50184; VWFC.1; 1.
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Xenoris laevis (African clawed frog).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
Xenopodinae; Xenopus.
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SEQUENCE 1486 AA; 142263 MW; 4A4A95772341042F CRC64;
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Sequence 243, Applications of the policy of

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Publication No. US20030064074A1

GENERAL INFORMATION:

APPLICANT: Chang, Robert C.

APPLICANT: Klvirikko, Kari I.

APPLICANT: Neff, Thomas B.

APPLICANT: Olsen, David R.

APPLICANT: Olsen, James W.

TITLE OF INVENTION: RECOMBINANT GELATINS IN VACCINES

FILE REPERENCE: FG0224

CURRENT FILING DATE: 2002-08-30

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CURRENT FILING DATE: 2002-08-30

PRIOR PILING DATE: 2000-11-10

NUMBER OF SEQ ID NOS: 33

SOFTWARE: Patentin Ver. 2.0

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2: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*
3: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep:*
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Copyright (c) 1993 - 2004 Compugen Ltd.
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Listing first 45 summaries
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                                                                                                                                      RESULT 2
US-10-104-889-16
Sequence 16, Application US/10104889
Sequence 16, Application US/10104889
Sequence 16, Application US/20040086961A1
GENERAL INFORMATION:
APPLICANT: GRUSKIN, ELLIOT A.
BROCKAW, JANE
ZHANG, GUANGHUI
STALE OF INVENTION: AMINO ACID MODIFIED POLYPEPTIDES
UNDERS. OF SEQUENCES: 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY: U.S.A.
ZIP: 11553
COMPUTER READALE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPATION: PERM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                               460 GSPGFQGLPGPAGPPGEAGKPGEQGVPGDLGAPGPSGARG 499
                                         GSPGFQGLPGPAGPPGEAGKPGEQGVPGDLGAPGPSGPAG 208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GSPGFQGLPGPAGPPGEAGKPGEQGVPGDLGAPGPSGARG 516
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93.6%; Pred. No. 1.4e-58;
tive 0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSE: DILWORTH & BARRESE
STREET: 333 EARLE OVINGTON BOULEVARD
CITY: UNIONDALE
STATE: NY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/104,889
FILING DATE: 22-Mar-2002
CLASSIFICATION: CURROW:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/169,768
ATTORNEY/AGENT TRORMATION:
NAME: STEEN, JEFFREY S
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: unknown
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 16:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEPHONE: (516) 228-8484
TELEFAX: (516) 228-8516
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 1057 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 93.6
Matches 206; Conservative
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297 GPPGPAGEEGKRGARGEPGPTGLPGPPGERGCPGSRGFPGADGVAGPKGPAGERGSPGPA 356
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 1057;
                                                                                                                                                                                PAOLELLA, DAVID
PAOLELLA, DAVID

ITTLE OF INDERTION: AMINO ACID MODIFIED POLYPEPTIDES
CORRESPONDENCE ADDRESS:
ADDRESSEE: DILMORTH & BARRESE
STREET: 333 EARLE OVINGTON BOULEVARD
CITY: UNIONDALE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               169 GSPGFQGLPGPAGPPGEAGKPGEQGVPGDLGAPGPSGPAG 208
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97.0%; Score 1149; DB 16;
Best Local Similarity 93.6%; Pred. No. 1.4e-58;
Matches 206; Conservative 0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/104,889
FILING DATE: 22-Mar-2002
CLASSTRICATION: «Unknown»
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US/09/169,768
FILING DATE: 09-OCT-1998
ATTORNEY/AGENT INFORMATION:
NAME: STEEN
TELECHONE: (516) 228-8484
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 20:
US-10-104-889-20
Sequence 20, Application US/10104889 Publication No. US20040086961A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-10-104-889-11; Sequence 11, Application US/10104889; Publication No. US20040086961A1; GENERAL INFORMATION:
                                                                        APPLICANT: GRUSKIN, ELLIOT A.
BUBCHTER, DOUGLAS
BROKAW, JANE
ZHANG, GUANGHUI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 1057 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                        ZIP: 11553
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: (516) 2:
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                      STATE: NY COUNTRY: U.S.A.
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49 GPKGSPGEAGRPGEAGLPGAKGLIGSPGSPGPDGKIGPPGPAGQDGRPGPPGAPGARGQA 108
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BROKAW, JANE
BROKAW, JANE
ZHANG, GUANGHUI
PROLELLA, DAVID
TITLE OF INVENTION: AMINO ACID MODIFIED POLYPEPTIDES
NUMBER OF SEQUENCES: 50
CORRESPONDENCE ADDRESS:
ADDRESSEE: DILMORTH & BARRESE
STREET: 333 EARLE OVINGTON BOULEVARD
CITY: UNIONDALE
STATE: NY
                                                                                                                                                                          COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC COMPATIBLE

APPLICATION DATA:

APPLICATION DATE: 22-Mar-2002

CLASSIFICATION: CURNOWN>

PRIOR APPLICATION: CURNOWN>

FILING DATE: 09-OCT-1998

ATTORNEY/AGENT INFORMATION:

NAME: STEEN, JEFFREY S

TELECOMMUNICATION: NORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GSPGFQGLPGPAGPPGEAGKPGEQGVPGDLGAPGPSGARG 516
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 97.0%; Score 1149; DB 16; Best Local Similarity 93.6%; Pred. No. 1.5e-58; Matches 206; Conservative 0; Mismatches 2;
                                                          ADDRESSEE: DILWORTH & BARRESE
STREET: 333 EARLE OVINGTON BOULEVARD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: unknown
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 6:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEPHONE: (516) 228-8484
TELEFAX: (516) 228-8516
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 1169 amino acids
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; Publication No. US20040086961A1
; GENERAL INFORMATION:
APPLICANT: GRUSKIN, ELLIOT A.
; BUECHTER, DOUGLAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: amino acid
STRANDEDNESS: single
                                                                                                     CITY: UNIONDALE STATE: NY
                                                                                                                                                          COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-10-104-889-8
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                                                                                                                                                                                                                                                                                                                                                COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC compatible
COMPUTER: IBM FC compatible
COMPUTER: Tale FC compatible
COMPUTER: Tale FC compatible
SOFTWARE: Patentin Release #1.0, Version #1.30
CURST APPLICATION NUMBER: US/10/104,889
FILING DATE: 22-Mar-2002
CLASSIFICATION NUMBER: US/09/169,768
ATTORNEY/AGENT INFORMATION:
NAME: STEERY STILING DATE: 09-0CT-1998
ATTORNEY/AGENT INFORMATION:
NAME: STEERY US/09/169,768
TELEFREY STILING DATE: 09-0CT-1998
ATTORNEY/AGENT INFORMATION:
TELEFREY (516) 228-8484
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-10-104-889-6; Application US/10104889; Sequence 6, Application US/10104889; Publication No. US20040086961A1; GENERAL INFORMATION: APPLICANT: GRUSKIN, ELLIOT A. BUECHTER, DOUGLAS BROKAW, JANE ZHANG, GUANGHUI PAOLELLA, DAVID; TITLE OF INVENTION: AMINO ACID MODIFIED POLYPEPTIDES;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2; Indels
APPLICANT: GRUSKIN, ELLIOT A.
BUEGHTER, DOUGLAS
BROKAW, JANE
EROKAW, GUANGHUI
PACLELLA, DAVID
TITLE OF INVENTION: AMINO ACID MODIFIED POLYPEPTIDES
NUMBER OF SEQUENCES: 50
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      477 GSPGFQGLPGPAGPPGEAGKPGEQGVPGDLGAPGPSGARG 516
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 97.0%; Score 1149; DB 16
Best Local Similarity 93.6%; Pred. No. 1.4e-58;
Matches 206; Conservative 0; Mismatches 2
                                                                                                                                                                                                        ADDRESSEE: DILWORTH & BARRESE
STREET: 333 EARLE OVINGTON BOULEVARD
CITY: UNIONDALE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRANDEDNESS: single
TOPOLOGY: unknown
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 11:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 1107 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: (516) 228-8
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                STATE: NY
COUNTRY: U.S.A.
ZIP: 11553
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49 GPKGSPGEAGRPGEAGLPGAKGLTGSPGSPGPDGKTGPPGPAGQDGRPGPPGPPGARGQA 108
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      109 GVMGFPGPKGAAGEPGKAGERGVPGPPGAVGPAGKDGEAGAQGPPGPAGPAGERGEQGPA 168
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TITLE OF INVENTION: AMINO ACID MODIFIED POLYPEPTIDES
NUMBER OF SEQUENCES: 50
CORRESPONDENCE ADDRESS:
ADDRESSES: DILMORTH & BARRESE
STREET: 333 BARLE OVINGTON BOULEVARD
CITY: UNIONDALE
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/058,124
FILING DATE: 29-Jan-2002
CLASSIFICATION: <UNKNOWN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    169 GSPGFQGLPGPAGPPGEAGKPGEQGVPGDLGAPGPSGPAG 208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      514 GSPGFQGLPGPAGPPGEAGKPGEQGVPGDLGAPGPSGARG 553
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     97.0%; Score 1149; DB 14;
93.6%; Pred. No. 1.7e-58;
ive 0; Mismatches 2;
                                                                                                                  PRIOR APPLICATION DATA:

APPLICATION NUMBER: 09/570,573
FILING DATE: 2002-MAY-12
APPLICATION NUMBER: 09/187,319
FILING DATE: <UNKNOWN-
ATTORNEY/AGENT INFORMATION:
NAME: GOGOTIS, Adda C
REGISTRATION NUMBER: 29,714
REFERENCE/DOCKET NUMBER: 29,714
TELECOMUNICATION INFORMATION:
TELECOMOMOTICATION INFORMATION:
TELECOMOMOTICATION INFORMATION:
TELECOMOMOTICATION INFORMATION:
TELEPHONE: 212-527-7700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLONE: COLLAGEN ALPHA 1 (1)
SEQUENCE DESCRIPTION: SEQ ID NO: 18:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 8
US-10-104-889-10
; Sequence 10, Application US/10104889
; Publication No. US20040086961A1
; GENERAL INFORMATION:
; APPLICANT: GRUSKIN, ELLIOT A.
BURGHTER, DOUGLAS
; BROKAW, JANE
ZHANG, GUANGHUI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ZIP: 11553
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Homo sapiens IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                    TELEX: 236687
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERICS:
LENGTH: 1341 amino a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: linear
MOLECULE TYPE: protein
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 93.6%
Matches 206; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STATE: NY COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-10-058-124-18
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APPLICANT: QVIST, Per
BONde, Martin
TITLE OF INVENTION: A Method for Assaying Collagen Fragments
in Body Fluids, A Test Kit and Means for Carrying Out the
Method and Use of the Method to Diagnose the Presence of
Disorders Associated with the Metabolism of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     49 GPKGSPGEAGRPGEAGLPGAKGLTGSPGSPGPDGKTGPPGPAGQDGRPGPPGPPGAKGQA 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   357 GPKGSPGEAGRPGEAGLPGAKGLTGSPGSPGPDGKTGPPGPAGQDGRPGPPGPPGAKGQA 416
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       109 GVMGFPGPKGAAGEPGKAGERGVPGPPGAVGPAGKDGEAGAQGPPGPAGPAGPAGERGEQGPA 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    417 GVMGFPGPKGAAGEPGKAGERGVPGPPGAVGPAGKDGEAGAOGPPGPAGPAGERGEOGPA 476
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 GPP------GEPGPTGLPGPPGERGGPGSRGFPGADGVAGPKGPAGERGSPGPA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          12; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 1171;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2; Indels
                                                                      MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/104,889
FILING DATE: 22-Mar-2002
CLASSIFICATION: <UNKNOWN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          477 GSPGFQGLPGPAGPPGBAGKPGEQGVPGDLGAPGPSGARG 516
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     169 GSPGFQGLPGPAGPPGBAGKPGEQGVPGDLGAPGPSGPAG 208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 97.0%; Score 1149; DB 16; Best Local Similarity 93.6%; Pred. No. 1.5e-58; Matches 206; Conservative 0; Mismatches 2;
                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/169,768
FILING DATE: 09-0CT-1998
ATTORNEY/AGENT INFORMATION:
NAME: STEEN, JEFFREY S
TELECOMMUNICATION INFORMATION:
TELEPHONE: (516) 228-6848
TELEFAX: (516) 228-6816
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY: USA
ZIP: 10022
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: unknown

NOLECULE TYPE: peptide

SEQUENCE DESCRIPTION: SEQ ID NO: 8:
US-10-104-889-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
ADDRESSEE: Darby & Darby PC STREET: 805 Third Avenue CITY: New York STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; Sequence 18, Application US/10058124; Publication No. US20030119058A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 1171 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
                          ZIP: 11553
COMPUTER READABLE FORM:
     COUNTRY: U.S.A.
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us-10-658-989a-1.rapb

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109 GVMGFPGPKGAAGEPGKAGERGVPGPPGAVGPAGKDGEAGAQGPPGPAGPAGERGEQGPA 168
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                                                                                                                                                                                                                                                                                        109 GVMGFPGPKGAAGEPGKAGERGVPGPPGAVGPAGKDGEAGAQGPPGPAGPAGERGEQGPA 168
                                                                                                                                                                                                                                                                                                                                                       575 GVMGFPGPKGAAGEPGKAGERGVPGPPGAVGPAGKDGEAGAQGPPGPAGPAGERGEQGPA 634
                                                                                       155 GPPGPAGEEGKRGARGEPGPTGLPGPPGERGGPGSRGFPGADGVAGPKGPAGERGSPGPA 514
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US-09-18-715-261
US-09-18-715-261
Sequence 261, Application US/09918715
Sequence 261, Application US/09918715
Sequence 261, Application US/09918715
Sequence 261, Application No. US20000017157A1
GENERAL INFORMATION:
APPLICANT: Brad St. Croix
APPLICANT: Renneth Kinzlen
TITLE OF INVENTION: ENDOFHELIAL CELL EXPRESSION PATTERNS
FILE REFERENCE: 1107.00134
CURRENT FALING DATE: 2001-08-01
PRIOR APPLICATION NUMBER: 60/225,599
PRIOR PLILING DATE: 2000-08-01
PRIOR PLILING DATE: 2000-08-11
PRIOR FILING DATE: 2000-08-11
PRIOR FILING DATE: 2000-08-11
PRIOR FILING DATE: 2000-08-11
SPRIOR FILING DATE: 2000-08-11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-10-060-036-159
Sequence 159, Application US/10060036
Sequence 159, Application US/10060036
Sequence 159, Application No. US20030073144A1
GENERAL INFORMATION:
APPLICANT: Benson, Darin R.
APPLICANT: Lodes, Michael D.
APPLICANT: Lodes, Michael U.
APPLICANT: Hepler, William T.
APPLICANT: Hepler, William T.
APPLICANT: Jang, Yuqiu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-918-715-261
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  49 GPKGSPGEAGRPGEAGLPGAKGLTGSPGSPGPDGKTGPPGPAGQDGRPGPPGPPGARGQA 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    109 GVMGPPGPKGAAGEPGKAGERGVPGPPGAVGPAGKDGEAGAQGPPGPAGPAGERGEQGPA 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  417 GVMGFPGPKGAAGEPGKAGERGVPGPPGAVGPAGKDGEAGAQGPPGPAGPAGERGEQGPA 476
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US-10-468-091-25

Sequence 25, Application US/10468091

Publication No. US200401573291

GENERAL INFORMATION:

APPLICANT: ADP Pharmaceutical Pty Limited

APPLICANT: The University of Sydney

TILLE OF INVENTION: Matrix gene expression in chondrogenesis

TILLE OF INVENTION: MATRIX gene expression in chondrogenesis

CURRENT FILING DATE: 2003-08-13

PRIOR APPLICATION NUMBER: US/10/468,091

CURRENT FILING DATE: 2003-08-13

PRIOR PEDICATION NUMBER: AU PR3116

PRIOR FILING DATE: 2001-02-15

NUMBER OF SEQ ID NOS: 42

SOFTWARE: PatentIn version 3.1

SEQ ID NO 25

IENGTH: 1461

TYPE: RR

CRAANISM: Homo sapiens

US-10-468-091-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 97.0%; Score 1149; DB 16; Length 1388; Best Local Similarity 93.6%; Pred. No. 1.7e-58; Matches 206; Conservative 0; Mismatches 2; Indels 12;
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/104,889
FILING DATE: 22-Mar-2002
CLASSIFICATION: <UNKnown>
PRIOR APPLICATION NUMBER: US/09/169,768
FILING DATE: 09-OCT-1998
ATTORION DATE: 109-OCT-1998
ATTORION NUMBER: US/09/169,768
FILING DATE: 09-OCT-1998
ATTORION DATE: 09-OCT-1998
ATTORION STEEN: US/09/169,768
FILING DATE: 09-OCT-1998
ATTORION STEEN: US/09/169,768
FILING DATE: 09-OCT-1098
ATTORION OF SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
TYPE: amino acids
TYPE: amino acids
TYPE: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GSPGFOGLPGPAGPPGEAGKPGEOGVPGDLGAPGPSGARG 516
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match . 97.0%; Score 1149; DB 16
Best Local Similarity 93.6%; Pred. No. 1.8e-58;
Matches 206; Conservative 0; Mismatches 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 10:
US-10-104-889-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GPP----
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517 108 577

458 GPPGPAGEEGKRGARGEPGPTGLPGPPGERGGPGSRGFPGADGVAGPKGPAGERGSPGPA 517

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Sequence 21, Application US/10216705
Sequence 21, Septement US20030096973A1
GENDIAGATION NO. US20030096973A1
APPLICANT: Meristem Therapeutics, S.A.
APPLICANTION: Recombinant Collagens and Derived Proteins Produced by Plants, Met
TITLE OF INVENTION: obtaining Such and Their Uses
FILE REFERENCE: 1149-3 DIV
CURRENT APPLICATION NUMBER: US 10/216,705
CURRENT FILING DATE: 2002-08-09
PRIOR APPLICATION NUMBER: US 09/331,347
NUMBER OF SEC ID NOS: 22
SOFTWARE: Patentin version 3.1
                                                              .49 GPKGSPGEAGRPGEAGLPGAKGLTGSPGSPGPDGKTGPPGPAGQDGRPGPPGPPGARGQA 108
                                                                                                                                                                          109 GVMGFPGPKGAAGEPGKAGERGVPGPPGAVGPAGKDGEAGAQGPPGPAGPAGERGEQGPA 168
                                                                                                                                                                                                                      578 GVMGFPGPKGAAGEPGKAGERGVPGPPGAVGPAGKDGBAGAGGPPGPAGPAGERGEQGPA 637
                                                                                                                       518 GPKGSPGEAGRPGEAGLPGAKGLTGSPGSPGPDGKTGPPGPAGQDGRPGPPGPPGARGQA
                                                                                                                                                                                                                                                                                              GSPGFQGLPGPAGPPGEAGKPGEQGVPGDLGAPGPSGPAG 208
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Pred. No. 1.8e-58;
0; Mismatches 2.
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TITLE OF INVENTION: ANTISENSE CLIGONUCLECTIDES
TITLE REFERENCE: 06275-254091
CURRENT APPLICATION NUMBER: US/10/149,352
CURRENT FILING DATE: 2002-06-10
PRIOR FILING DATE: 2000-12-12
PRIOR FILING DATE: 2000-12-12
PRIOR APPLICATION NUMBER: GB 9929487.8
PRIOR PLING DATE: 1999-12-15
NUMBER OF SEQ ID NOS: 14
SOFTWARE: Patentin Ver. 4.0
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Publication No. US20030105050A1
GENERAL INFORMATION:
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US-10-216-705-21
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TYPE: PRT
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US-10-149-352-2
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  INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY INVENTION: AND DIAGNOSIS OF PANCREATIC CANCER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
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93.6%; Pred. No. 1.8e-58;
tive 0; Mismatches 2;
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TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITTLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITTLE OF INVENTION: DENTIFECATION, ASSESSMENT, TITLE OF INVENTION: DENTIFECATION, ASSESSMENT, TITLE OF INVENTION: OF CREVICAL CANCER
FILE REFERENCE: MRI-035
CURRENT APPLICATION NUMBER: US, 60/298, 159
PRIOR FILING DATE: 2001-06-13
PRIOR FILING DATE: 2001-06-13
PRIOR FILING DATE: 2001-06-13
PRIOR APPLICATION NUMBER: US, 60/298, 155
PRIOR APPLICATION NUMBER: US, 60/298, 155
PRIOR FILING DATE: 2001-06-13
PRIOR FILING DATE: 2001-10-114
NUMBER: OF SEQ ID NOS: 238
SOFTWARE: FRAGSEQ for Windows Version 4.0
SEQ ID NOS: 238
TITLE OF INVENTION: COMPOSITIONS AND METHO
TITLE OF INVENTION: AND DIAGNOSIS OF PANC
FILE REFERENCE: 210121.566
CURRENT APPLICATION NUMBER: US/10/060,036
CURRENT FILING DATE: 2002-01-30
NUMBER OF SEQ ID NOS: 4560
SOFTWARE: FASLESQ for Windows Version 4.0
SEQ ID NO 159
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Schlegel, Robert
APPLICANT: Chen, Yan
APPLICANT: Ano, Xumei
APPLICANT: Monahan, John
APPLICANT: Ramatkar, Shubhangi
APPLICANT: Galatt, Karen
APPLICANT: Gannayarapu, Manjula
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Best Local Similarity 93.64
Matches 206; Conservative
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49 GPKGSPGEAGRPGEAGLPGAKGLTGSPGSPGPDGKTGPPGPAGQDGRPGPPGARGQA 108 109 GVMGFPGPKGAAGEPGKAGERGVPGPPGAVGPAGKDGEAGAQGPPGPAGPAGPAGERGEQGPA 168 48 1 GPP-----GEPGPTGLPGPPGERGGPGSRGFPGADGVAGPKGPAGERGSPGPA 518 GPKGSPGEAGRPGEAGLPGAKGLTGSPGSPGPDGKTGPPGPAGQDGRPGPPGPPGARGQA 458 GPPGPAGEEGKRGARGEPGPTGLPGPPGERGGPGSRGFPGADGVAGPKGPAGERGSPGPA 12; Gaps Indels 169 GSPGFQGLPGPAGPPGEAGKPGEQGVPGDLGAPGPSGPAG 208 638 GSPGFOGLPGPAGPPGEAGKPGEOGVPGDLGAPGPSGARG 677 108

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                                           Query Match

97.0%; Score 1149; DB 14; Length 1464;
Best Local Similarity 93.6%; Pred. No. 1.8e-58;
Matches 206; Conservative 0; Mismatches 2; Indels 12;
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APPLICANT: Meyers, Kachert C.
APPLICANT: Hortobagyi, Gabriel N.
APPLICANT: Hortobagyi, Gabriel N.
APPLICANT: Puaztai, Lajos
APPLICANT: Puaztai, Lajos
APPLICANT: Main, Aysegul
APPLICANT: Mila, Gordon B.
TITLE OF INVENTION: COMPOSITIONS, KITS, AND METHODS FOR IDENTIFICATION, ASSESSMENT,
TITLE OF INVENTION: COMPOSITIONS, KITS, AND METHODS FOR IDENTIFICATION,
TITLE OF INVENTION: COMPOSITIONS, KITS, AND METHODS FOR IDENTIFICATION,
TITLE OF INVENTION: COMPOSITIONS, KITS, AND METHODS FOR IDENTIFICATION,
TITLE OF INVENTION: COMPOSITION, AND THERAPY OF BREAST CANCER
TITLE OF INVENTION: DATE: 2002-06-21
PRIOR FILING DATE: 2001-06-21
PRIOR FILING DATE: 2001-06-27
PRIOR FILING DATE: 2001-09-25
PRIOR FILING DATE: 2001-09-25
PRIOR FILING DATE: 2001-09-25
PRIOR FILING DATE: 2002-03-05
PRIOR FILING DATE: 2002-03-05
PRIOR FILING DATE: 2002-03-05
PRIOR FILING DATE: 2002-03-05
PRIOR FILING DATE: 2002-05-14
NUMBER OF SEQ ID NOS: 506
SOFTWARE: FastSEQ for Windows Version 4.0
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Publication No. US20030124128A1
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Gannavarpu, Manjula
Kamatkar, Shubhangi
Mertens, Maureen
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Hoersch, Sebastian
Monahan, John
Meyers, Rachel E.
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Wang, Youzhen
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ORGANISM: Homo sapiens
                             LENGTH: 1464
TYPE: PRT
CRGANISM: Homo sapiens
US-10-149-352-2
     SEQ ID NO 2
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US-10-658-989A-1 1184 1 GPPGEFGPTGLFGPPGERGG......GEQGVPGDLGAPGFSGPAGG 209

BLOSUM62 Gapop 10.0 , Gapext 0.5 Title: Perfect score: Sequence: Scoring table:

141681 segs, 52070155 residues Searched: 141681 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt_42:* Database : Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

1	-	Description		homo sa	rattus	mus m	gall	bost	homo	u snu	pos	gallı	рошо		rattı	EUM.	goq	MUS.	pog.		cani	rana	onco	gallu	P30754 riftia pach	DOMO.	homo	mus mu	_	canis	bos tal	gailus	gallus	homo s	. rattus
SUMMARIES		OI OI	CA11 CANFA	CA11 HUMAN	CA11_RAT		CA11_CHICK	CA12 BOVIN	CA12 HUMAN	CA12_MOUSE	CA11 BOVIN	CA13_CHICK	CA25_HUMAN	CA13_HUMAN	CA21_RAT	CA13 MOUSE	CA13_BOVIN	CA21 MOUSE	CA21_BOVIN	CA21 HUMAN	CA21 CANFA	CA21_RANCA	CA21_ONCMY	CA21_CHICK	CAFF RIFPA	CA15_HUMAN	CA2B_HUMAN	CA2B_MOUSE					اما	44_HU	CA13_RAT
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CA39_HUMAN CA35_HUMAN	CA17_HUMAN	CAIF HUMAN CAI9 HUMAN CAIA CHICK	CAIA_HUMAN CA21_RABIT CA19_MOUSE	CA24_HUMAN
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MEDLINE-84270697; PubMed-8462220;
Chu M.-L., de Wet W.J., Bernard M.P., Ding J.-F., Morabito M.,
Myers J., Williams C., Ramirez F.,
"Human pro alpha 1(1) collagen gene structure reveals evolutionary
conservation of a pattern of introns and exons.";
Nature 310:337-340(1984)
                                                                         NONHELICAL REGION (N-TERMINAL).
TRIPLE-HELICAL REGION.
NONHELICAL REGION (C-TERMINAL).
CELL ATTACHMENT SITE (POTENTIAL).
CELL ATTACHMENT SITE (POTENTIAL).
N-LINKED (GLCRAC...) (POTENTIAL).
G-> A (in OI; severe).
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
MCBI_TaxID=9606;
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MEDLINES-8902564; PubMed=1178743;
Tromp G., Kuivanieni H., Stacey A., Shikata H., Baldwin C.T.,
Jaenisch R., Prockup D.J.;
"Structure of a full-length cDNA clone for the prepro alpha 1(1)
chain of human type I procollagen.";
Biochem. J. 253:319-922(1988)
                                                                                                                                                                                                                                       Score 1149; DB 1; Length 1460;
Pred. No. 4.1e-48;
0; Mismatches 2; Indels 12
                     COLLAGEN ALPHA 1(I) CHAIN,
CARBOXYL-TERMINAL PROPEPTIDE.
VWFC.
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138762 MW; 58E3674D2B570697 CRC64;
     AMINO-TERMINAL PROPEPTIDE
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10-NMR-1989 (Rel. 0), Created)
10-CCT-2003 (Rel. 10, Last sequence update)
Collagen alpha 1(1) chain precursor.
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MEDLINE=71038625; PubMed=5529814;
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SEQUENCE OF 263-268.
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SEQUENCE OF 425-1464 FROM N.A.
MEDLINE=64080385; PubMed=6689127;
Bernard M.P., Chu M.-L., Myers J.C., Ramirez F., Eikenberry E.F.,
Prockop D.J.;
"Nucleotide sequences of complementary deoxyribonucleic acids for the
pro alpha I chain of human type I procollagen. Statistical evaluation
of structures that are conserved during evolution.";
Hiochemistry 22:5213-5223 (1983).
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MEDLINE=91184577; PubMed=2010058;
Kuivaniemi H., Tromp G., Prockop D.J.;
"Mutations in collagen genes: causes of rare and some common diseases in humans.";
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MEDLINE=88097389; PubMed=3480516;

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Maekelae J.K., Raassina M., Virta A., Vuorio E.;
"Human pro alpha 1(I) collagen: cDNA sequence for the C-propeptide
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J. Med. Genet. 28:433-442(1991).
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MEDILINE=85130970; PubMed=2857713;
MEDILINE=85130970; PubMed=2857713;
MEDILINE=85130970; PubMed=2857713;
MEDILINE=85130970; PubMed=2867713;
Fine structural analysis of the human pro-alpha 1 (I) collagen grouncter structure, Alul repeats, and polymorphic transcripts.";
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"The human type I collagen mutation database.";
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                                                                                                                                                formation.";
J. Biol. Chem. 245:5042-5048(1970)
MEDLINE=71001508; PubMed=4319110;
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MEDLINE=91374476; PubMed=1895312;
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MEDLINE=97169389; PubMed=9016532;
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SEQUENCE OF 1229-1454 FROM N.A.
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
"A lethal variant of osteogenesis imperfecta has a single base mutation that substitutes cysteine for glycine 904 of the alpha 1(I) chain of type I procollagen. The asymptomatic mother has an unidentified mutation producing an overmodified and unstable type I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=67162268; PubMed=5337886;
Kang A.H., Bornstein P., Piez K.A.;
"The amino acid sequence of peptides from the cross-linking region
                                                                                                                                                                                                                                                                                                                                                                                      for glycine 1(I) chains
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VARIANTS OI CYS-272; CYS-704 AND CYS-896.

WEDLINES-90009313; PubMed=2794057;

Starman B.J., Eyre D., Charbonneau H., Harrylock M., Weis M.A.,

Weiss L., Graham J.M., Byers P.H.;

Weiss L., Graham J.M., Byers P.H.;

"Osteogenesis imperfecta. The position of substitution for glyc:

Cysteine in the triple helical domain of the pro alpha 1(I) cha

type I collagen determines the clinical phenotype.";
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93.6%; Pred. No. 4.1e-48;
tive 0; Mismatches 2;
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The absence of a short sequence at
                                                                                                                                            procollagen.";
J. Clin. Invest. 83:574-584(1989).
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MEDLINE=67165368; PubMed=4290711;
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Siochemistry 6:788-795(1967)
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Best Local Similarity 93.6
Matches 206; Conservative
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MEDIANE=90062068; PubMed=2511192;
Pack W. Constantiou C.D., Kalia K., Nielsen K.B., Prockop D.J.;
Pack W. Constantiou of or alpha 1(I)-glycine 844 in a severe
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helix of type I procollagen. The effects of glycine substitutions on
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"Lethal perinatal osteogenesis imperfecta due to the substitution of arginine for glycine at residue 391 of the alpha 1(1) chain of type I
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Patterson E., Smiley E., Bonadio J.;
"RNA sequence analysis of a perinatal lethal osteogenesis imperfecta
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MEDIATE=8829828; PubNed=3403550;
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the peptide defect by in vitro expression of the mutant cDNA.";
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WINDIAMES BO33031, PubMed=3667599;
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WOGGL B.E., Minor R.R., Freund M., Prockop D.J.;
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of the alpha I chain to cysteine and destabilizes the triple helix
a lethal variant of osteogenesis imperfecta.";
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MEDLINE=99218628; PubMed=3244312;
MEDLINE=99218628; PubMed=3244312;
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"A cysteine for glycine substitution at position 1017 in an alpha 1(1) chain of type I collagen in a patient with mild dominantly inherited osteogenesis imperfecta.";
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                                                                                                                                                        nucleotide
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MEDLINE=89380165; PubMed=2777764;
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MEDLINE-89109573; PubMed=2913053;
Constantinou C.D., Nielsen K.B., Prockop D.J.;
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J. Biol. Chem. 262:7021-7027(1987)
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Butler W.T.;

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DR InterPro; IPR008161; Collagen.

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MOD_RES 47 HYDROXYLATION (PROBABLE).

"TROXYLATION (PROBABLE)
                                                                                                                 use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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MEDLINE=85122694; PubMed=6395893;
MEDLINE=86122694; PubMed=6395893;
"Construction of DNA sequences complementary to rat alpha 1 and alpha "construction of DNA sequences complementary to rat alpha 1 and alpha 2 collagen mank and their use in studying the regulation of type I class not supplementary 23:6210-6216 (1984).

Biochemistry 23:6210-6216 (1984).

-: FUNCTION: Type I collagen is a member of group I collagen
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Ballan G., Click E.M., Bornstein P.;
"Structure of rat skin collagen alpha 1-CB8. Amino acid sequence of the hydroxylamine-produced fragment HA1.";
Biochemistry 10:4470-4478(1971).
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MEDLINE=73006942; PubMed=4342027;
Balian G., Click E.M., Hermodson M.A., Bornstein P.;
"Structure of rat skin collagen alpha 1-CBB. Amino acid sequence the hydroxyl amine-produced fragment HA2.";
Biochemistry 11:3798-3806(1972);
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MEDLINE=71263178; PubMed=4327399;
Butler W.T., Ponds S.L.,
"Chemical studies on the cyanogen bromide peptides of rat skin collagen. Amino acid sequence of alpha 1-CB4.";
Blochemistry 10:2076-2081(1971).
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Structural and immunogenic properties of a major antigenic
determinant in neutral salt-extracted rat-skin collagen.";
Eur. J. Biochem. 37:287-294(1973).
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MEDLINE=73049455; PubMed=4636751;
Stooltz M., Timpl R., Kuehn K.;
"Non-helical regions in rat collagen alpha 1-chain.";
FEBS Lett. 26:61-65(1972).
                                                                                                       Chem. 242:2572-2574(1967)
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Gaps

DB 1; Length 671; 5; Indels 48

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MEDLINE-96033240; PubMed=8535610;
Li S.W., Khillan J., Prockop D.J.;
"The complete cDNA coding sequence for the mouse pro alpha 1(1) chain
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
GSPGFQGLPGPAGPPGEAGKPGZZGVPGDLGAPGPSGARG
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Matrix Biol. 14:593-595(1995).
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rix; Connective tissue; Repeat; Hydroxylation;
PROSITE; PS50184; VWFC 2; 1.
Extracellular matrix; Connective Glycoprotein; Collagen; Signal.
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MDDINESBR124776; PubMed=3340560;
MOOSlehner K., Harbers K., Harbers K., Harbers K.,
"Two mrNas of mouse pro alpha 1(1) collagen gene differ in the size
of the 3'-untranslated region.";
Nucleic Acids Res. 16:773-773(1988).
-1- PUNCTION: Type I collagen is a member of group I collagen
                                                                                                                                                                                    Monson J.M., Friedman J., McCarthy B.J.;
"DNA sequence analysis of a mouse pro alpha 1 (I) procollagen gene:
evidence for a mouse B1 element within the gene.";
Mol. Cell. Biol. 2:1362-1371(1982).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (fibrillar forming collagen).
--- SUBUNIT: Trimers of one alpha 2(I) and two alpha 1(I) chains.
--- TISSUE SPECIFICITY: Forms the fibrils of tendon, ligaments and bones. In bones the fibrils are mineralized with calcium
                                                                                                                                                                                                                                                                                                                Monson J.M., McCarthy B.J.;
"Identification of a Balb/c mouse pro alpha 1(1) procollagen gene evidence for insertions or deletions in gene coding sequences.";
DNA 1:59-69(1981).
                          SEQUENCE OF 518-1128 FROM N.A.
MEDLINE=86137403, PubMed=3841523,
French B. T., Lee W. H., Maul G.G.;
French B. T., Lee W. H., Maul G.G.;
Fivench B. T., Lee Conserve of a cDNA clone for mouse pro alpha 1(I)
                                                                                                                                                                                                                                                                                        SEQUENCE OF 735-878 AND 1005-1058 FROM N.A MEDLINE=83157109; PubMed=6219867;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR008161; Clg helix.
InterPro; IPR008160; Colladen.
InterPro; IPR00160; Fibzingen_C.
InterPro; IPR001801; Fibzingen_C.
InterPro; IPR001007; VWF_C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Probom; PD000007; CIG_Helix; 1.
Probom; PD002078; Fib_collagen_C; 1.
SMART; SM00038; COLFI; 1.
PROSITE; PS01208; VWC; 1.
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AAA37332.1; JOINED.
AAA37332.1; JOINED.
AAA37332.1; JOINED.
                                                                                                                                                        SEQUENCE OF 735-1130 FROM N.A. MEDLINE=83141374; PubMed=6298597;
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AAA37332.1; JOINED
AAA37332.1; JOINED
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Pfam; PF01391; Collagen; 18.
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                                                                                                    collagen protein.";
Gene 39:311-312(1985).
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EMBL;
PIR; S
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Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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Highberger J.H., Corbett C., Dixit S.N., Yu W., Seyer J.M.,
Kang A.H., Gross J.;
"Amino acid sequence of chick skin collagen alpha 1(1)-CB8 and the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDIINE-88056316; PubMed-3678834;
Finer M.H., Boedtker H., Doty P.;
"Construction and characterization of cDNA clones encoding the 5'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE OF 1-144 FROM N.A.

MEDLINE=88007542; PubMed-2820966;
Finer M.H., Aho S., Gerstenfeld L.C., Boedtker H., Doty P.;
Finer M.H., Aho S., Gerstenfeld M.C., Boedtker H., Doty P.;
Finer M.H., Aho S., Gerstenfeld M.C., Boedtker Tegion and the first intron of the chicken pro-alpha 1(1) collagen gene.";
J. Biol. Chem. 262:13323-13332 (1987).
                                                                                          VWFC.
NONHELICAL REGION (N-TERMINAL).
TRIPLE-HELICAL REGION.
NONHELICAL REGION. (C-TERMINAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              12;
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Pred. No. 1.5e-46;
                                                                                                                                                                                                                                                                             36 CELL ATTACHMENT SITE (POTENTIAL)
84 CELL ATTACHMENT SITE (POTENTIAL)
50 A -> V (IN REF. 5).
137944 MW; 38802E535DF81808 CRC64;
AMINO-TERMINAL PROPEPTIDE.
COLLAGEN ALPHA 1(I) CHAIN.
CARBOXYL-TERMINAL PROPEPTIDE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5; Indels
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Gene 56:71-78(1987).
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01-0CT-1989 (Rel. 12, Last sequence update)
01-0CT-2003 (Rel. 42, Last annotation update)
Collagen alpha 1(1) chain precursor.
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SOLUTION
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                                             [4]
SEQUENCE OF 1200-1205.
MEDIINE-72243016; PubMed=5047697;
Eyre D.R., Glimcher M.J.;
"Evidence for a previously undetected sequence at the carboxyterminus of the alpha 1 chain of chicken bone collagen.";
Blochem. Blophys. Res. Commun. 48:720-726(1972).
                                                                                                                                                                                             Fuller F., Boedtker H.; "Sequence determination and analysis of the 3' region of chicken proapplant (1) and pro-alpha 2(1) collagen messenger ribonucleic acids including the carboxy-terminal propeptide sequences."; Biochemistry 20:996-1006(1981).
complete primary structure of the helical portion of the chick skin collagen alpha 1(I) chain.";
Biochemistry 21:2048-2055(1982).
                                                                                                                                                                                                                                                                                   SEQUENCE OF 1311-1453 FROM N.A.

MEDLINE=80134546; PubMed=6987088;
Showalter A.M., Pesciotta D.M., Eikenberry E.F., Yamamoto T.,
Pastan I., Decrombrugghe B., Fietzek P.E., Olsen B.R.;
"Nucleotide sequence of a collagen cDNA-fragment coding for the
"Nucleotide sequence of a collagen cDNA-fragment coding for the
"Nucleotide sequence of a collagen cDNA-fragment coding for the
"Nucleotide sequence of a collagen cDNA-fragment coding for the
FEBS Lett. 111:61-65(1980).
-!- FUNCTION: Type I collagen is a member of group I collagen
(fibrillar forming collagen).
-!- SUBUNIT: Trimers of one alpha 2(I) and two alpha 1(I) chains.
-!- TISSUE SPECIFICITY: Forms the fibrils of tendon, ligaments and
bones. In bones the fibrils are mineralized with calcium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PTM: Proline residues at the third position of the tripeptide repeating unit. (G-X-Y) are hydroxylated in some or all of the chains: Pro-1153 is the only 3-hydroxypro and the only hydroxylated proline in position. SIMILARITY: Contains 1 WWPC domain.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AMINO-TERMINAL PROPEPTIDE. COLLAGEN ALPHA 1(1) CHAIN. C-TERMINAL PROPEPTIDE.
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Interprof. TPR008161; Clg helix.
Interprof. IPR008169; Collagen.
Interprof. IPR00181; Fib_collagen_C.
Interprof. IPR001007; WWF_C.
Pfam, PF01410; CCLF1; 1.
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EMBL, MI7839; AAA48704.1; -
EMBL, WO0401; CAA23695.1; -
EMBL, MI0571; AAA48671.1; ALT_SEQ.
EMBL, MI7677; AAA48672.1; -
EMBL, MI7677; AAA48672.1; -
PIR, X27179; A27179.
                                                                                                                                                                SEQUENCE OF 981-1453 FROM N.A. MEDLINE=81160715; PubMed=6927845;
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151
1205
1453
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108
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"Isolation and characterization of the cyanogen bromide peptides from the alpha 1(II) chain of bovine and human cartilage collagen.";
Biochemistry 12:3153-3159(1973).
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MBDLINE=76255504; PubMed=782511;
Butler W.T., Miller E.J., Finch J.E. Jr.;
But let W.T. willer tructure of cartilage collagen. Amino acid sequence of the NH2-terminal helical portion of the alpha 1 (II) chain.";
Biochemistry 15:3000-3006 (1976).
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"The covalent structure of cartilage collagen. Bvidence for sequence
hererogeneity of bovine alpha!(II) chains.";
J. Biol. Chem. 252:639-643(1977).
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Bukaryota, Metazoa; Chordata, Craniata, Vertebrata, Buteleostomi;
Mammalia, Eutheria, Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Bovinae; Bos.
                                                                                                                                                                                                                                                                                          12;
                                                                                                                                                                                                                                             DB 1; Length 1453;
                                                                                                                                                                                                                                                                                       14; Indels
                                                                                                                                                     17 F -> L (IN REF. 5).
11 Q -> H (IN REF. 6).
137789 MW; 3BC6152134271F4D CRC64;
                    PYRROLIDONE CARBOXYLIC ACII
HYDROXXLATION (POTENTIAL)
HYDROXXLATION (POTENTIAL)
HYDROXXLATION (POTENTIAL)
HYDROXXLATION (POTENTIAL)
HYDROXXLATION (POTENTIAL)
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                                                                                                                                                                                                                                           Score 1067; DB 1
Pred. No. 3e-44;
                                                                                                                                                                                                                                                                                       4; Mismatches
                                                                                                                                    HYDROXYLATION.
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TISSUB=Cartilage;
MEDLINE=73258693; PubMed=4732855;
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MEDLINE=77093864; PubMed=833147;
                                                                                                                                                                                                                                             90.1%;
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152
254
851
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1153
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                                                                                                                                                                                                                                                                  Similarity
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152
254
1081
1097
1153
1153
1441
DOMAIN
MOD RES
MOD RES
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CA12 BOVIN
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121 GEPGKAGERGVPGPPGAVGPAGKDGEAGAQGPPGPAGPAGERGEQGPAGSPGFQGLPGPA 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCSI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       [2]
SEQUENCE OF 1-28 FROM N.A.
MEDLINE=87031574; PubMed=3021582;
Nunez A.M., Kohno K., Martin G.R., Yamada Y.;
"Promoter region of the human pro-alpha 1(II)-collagen gene.";
Gene 44:11-16(1986).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                21_JUL-1986 (Rel. 01, Created)
01-JAN-1990 (Rel. 13, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
COLLAGen alpha 1(II) chain precursor [Contains: Chondrocalcin]
                                                                                                                                                                                                                                     L -> A (IN MINOR COMPONENT).

Q -> L (IN MINOR COMPONENT).

G -> Z (IN REF. 3).

AP -> PA (IN REF. 3).

EA -> AS (IN REF. 3).

T -> Q (IN REF. 4).

S -> A (IN REF. 4).
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                                                                                                                                                                                                                                                                                                                                                    T -> Q (IN REF. 4).
S -> A (IN REF. 4).
P -> A (IN REF. 4).
Q -> T (IN REF. 4).
Q -> T (IN REF. 4).
Q -> T (IN REF. 4).
G -> P (IN REF. 5).
G -> P (IN REF. 5).
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                                                            HYDROXYLATION.
O-LINKED (GAL.
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Nucleic Acids Res. 17:9473-9473(1989).
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The Calf type II collagen.";

In Nucleic Acids Res. 13:2815-2826 (1985)

In SUBUNIT: Homotrimers of alpha 1(II) chains.

In SUBUNIT: Homotrimers of alpha 1(II) chains.

In Puncleic Acids Res. 13:2815-2826 (1985)

In Proparating unit (G-X-Y) are hydroxylated in some or all of the chains. Hydroxylation on Pro-9 is involved in cross-linking.

In Proparating unit (G-X-Y) are hydroxylated in some or all of the chains. Hydroxylation on Pro-9 is involved in cross-linking.

In Proparating atom of post-translationally added hydroxyl groups.

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InterPro; IPR000160; Collagen.
InterPro; IPR001607; Collagen.
InterPro; IPR001007; VWF C.
ProDom; PD000007; Clg_helix; 2.
ProDom; PD002078; Fib_collagen_C; 1.
SMART; SM00008; ColFT; 1.
PROSITE; PS01208; VWFC_1; PARIIAL.
Extracellular matrix; Connective tissue; Repeat; Hydroxylation;
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Ramirez F.;
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                                                                                                          Eur. J. Biochem. 181:159-173(1989)
                                                                                                                                                                                                                                                                                                   SEQUENCE OF 180-272 FROM N.A.
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MEDLINE=86104139; PubMed=3002437;
Whorez A.M., Francomano C., Young M.F., Martin G.R., Yamada Y.;
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MEDLINE-89233138; PubMed=2714801;
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VARIANT SEMD ARG-285.
MEDLINE=93252400; PubMed=8486375;
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                                                                                                       WEDLINE=94063862; PubMed=8244341; Williams C.J., Considine E.L., Knowlton R.G., Reginato A., Neumann Williams C.J., Considine E.L., Knowlton R.G., Reginato A., Neumann Harrison D., Buxton P., Jimenez S.A., Prockop D.J.; Spondyloepiphyseal dysplasia and precocious osteoarthritis in a family with an Arg75-->Cys mutation in the procollagen type II gene (COLZAI).";
                                           type
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                                            MEDLINE=93315508; PubMed=8325895;
Chan D., Taylor T.K.F., Cole W.G.;
"Characterization of an arginine 789 to cysteine substitution in
alpha 1 (II) collagen chains of a patient with spondyloepiphyseal
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"Mouse type II collagen gene. Complete nucleotide sequence, exon
"tructure, and alternative splicing";
J. Biol. Chem. 266.18862-16869(1991).
Vikkula M., Ritvaniemi P., Vuorio A.F., Kaitila I., Ala-Kokko L.,
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01-DEC-1992 (Rel. 24, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
Collagen alpha 1(II) chain precursor [Contains: Chondrocalcin]
                      Peltonen L.;
"A mutation in the amino-terminal end of the triple helix of collagen causing severe osteochondrodysplasia.";
Genomics 16:282-285(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          72.8%; Score 862; DB 1; Length 1418; 74.0%; Pred. No. 1.4e-34; ive 11; Mismatches 43; Indels C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING. MEDLINE=91358489; PubMed=1885613;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT; 1459 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                     dysplasia.";
J. Biol. Chem. 268:15238-15245(1993)
                                                                                                                                                                                                                                                                                Genet. 92:499-505(1993)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      154; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VARIANT SEDC SER-1128
                                                                                                                                                                                                                                                                                                                            VARIANT SEDC CYS-920.
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P28481;
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the BWBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                           collagen mRNAs.";
Biochim. Biophys. Acta 1089:241-243(1991).
-!- FUNCTION: Collagen type II is specific for cartilaginous tissues.
-!- SUBDNIT: Homotrimers of alpha 1(II) chains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                            Isold=P28481-2; Sequence=VSP 001139, VSP_001140;
-!-PTM: Prolines at the third position of the tripeptide repeating unit (G-X-Y) are hydroxylated in some or all of the chains.
-!- SIMILARITY: Contains 1 VWFC domain.
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SEQUENCE OF 1455-1459 FROM N.A.
MEDILTNE-91274355, PubMed-2054384;
Metsaranta M., Toman D., de Crombrugghe B., Vuorio E.;
"Specific hybridization probes for mouse type I, II, III and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 1459;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NONHELICAL REGION (C-TERMINAL)
Q -> R (in isoform Short).
/FTId=VSP_001139.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 839; DB 1; Length 14; Pred. No. 1.7e-33; 12; Mismatches 46; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Missing (in isoform Short). /FIId=VSP_001140.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TRIPLE-HELICAL REGION.
                                                                                                                                                                                                          Event=Alternative splicing; Named isoforms=2;
                                                                                                                                                                                                                                            IsoId=P28481-1; Sequence=Displayed;
Name=Short;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MGD, MGI 88452, CO1221.
InterPro; IPRO08161; Clg helix.
InterPro; IPR008160; Collagen.
InterPro; IPR00885; Fib collagen.
InterPro; IPR001007; VWF_C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pfam; PF01410; COLFI; 1.
Pfam; PF01391; Collagen; 18.
Pfam; PF00031; vvc. 1.
ProDom; PD000007; Clg helix;
ProDom; PD002078; Fib_collage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; M65161; AAA68100.1; -. EMBL; X57982; CAA41047.1; -.
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Best Local Similarity 72.1
Matches 150; Conservative
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1186
1213
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hydroxyapatite. Properties the third position of the tripeptide PTM: Proline residues at the third position of the repeating unit (G-X-Y) are hydroxylated in some or all of the chains. Pro-726 is the only 3-hydroxypro and the only hydroxylated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Rauterberg J., Timpl R., Furthmayr H.; "Structural characterization of N-terminal antigenic determinants in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=73049499; PubMed=4673951;
Fietzek P.P., Wendt P., Kell I., Kuehn K.;
"The covalent structure of collagen: amino acid sequence of alpha-1-
CB3 from calf skin collagen.";
FEBS Lett. 26:74-76(1972).
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SEQUENCE OF 676-751.

PIBELINE-73042275, PubMed-4343807,

Fietzek F.P., Rexrodt F.W., Wendt P., Stark M., Kuehn K.,

"The covalent structure of collagen. Amino-acid sequence of peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE OF 20-145.
MEDLINE-76022320; PubMed=1164916;
MEDLINE-76022320; PubMed=1164916;
MEDLINE-76022320; Ruchn K.;
"The covalent structure of collagen: amino-acid sequence of the cyanogen-bromide peptides alpha-1-CB2, alpha-1-CB4 and alpha-1-CB5 from calf-skin collagen.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Cetartiodactyla, Ruminantia, Pecora, Bovoldea,
Boyidae, Bovinae, Bos.
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-1- SUBUNIT: Trimers of one alpha 2(I) and two alpha 1(I) chains.
-1- TISSUE SPECIFICITY: Forms the fibrils of tendon, ligaments and bones. In bones the fibrils are mineralized with calcium
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MEDLINE=74086118; PubMed=4359390;
Fierzek P.P., Rexrodt F.W., Hopper K.E., Kuehn K.;
"The covalent structure of collagen. 2. The amino-acid sequence alpha-1-GB7 from calf-skin collagen.";
Eur. J. Biochem. 38:396-400(1973).
                                                                                                                                                                                                                                                                                                  21-JUL-1986 (Rel. 01, Created)
01-FEB-1994 (Rel. 28, Last sequence update)
11-MAR-2004 (Rel. 43, Last annotation update)
Collagen alpha 1(1) chain (Fragments).
                                                                                                                                                                                                                                      779 AA
                                       644 GPPGEGGKQGDQGIPGEAGAPGLVGPRG
   GPPGEAGKPGEQGVPGDLGAPGPSGPAG
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MEDLINE=72255334; PubMed=4115172;
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Eur. J. Biochem. 30:169-183(1972)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               human collagen.";
                                                                                                                                                                                                                                      STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bos taurus (Bovine)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=9913;
                                                                                                                                                                                                                                  BOVIN
   181
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                                                                                                                                                            RESULT 9
CA11 BOVIN
CA12 BOVIN
CA12 BOVIN
DIT 21-7UL-
DIT 01-FEB-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  149 GPKGAAGEPGKAGERGVPGPPGAVGPAGKDGEAGAQGPPGPAGPAGERGEQGPAGSPGFQ
                                                                                         -!- MISCELLANGEOUS...

IRE, A91193; CGEOIS...

IREPTO, IPRO08161; C1g helix.

InterPro; IPR008161; Collagen.

InterPro; IPR001007; VWF C.

PRODOM; PD000007; C1g helix; 1.

PROSITE; PS01208; VWFC 1; PARTIAL.

Extracellular matrix; Connective tissue; Repeat; Hydroxylation; dlycoprotein; Collagen; Pyrrolidone carboxylic acid.

MOD RES

MOD RES

9 CONVERTED TO AN ALDEHYDE GROUP THAT IS CONVERTED

MOD_RES

9 CONVENTED TO AN ALDEHYDE GROUP THAT IS CONVENTED.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      55 GEAGRPGEAGLPGAKGLTGSPGSPGPDGKTGPPGPAGQDGRPGPPGPPGARGQAGVMGFP
proline in position X.
-!- PTM: O-linked glycan consists of a Glc-Gal disaccharide bound to the oxygen atom of a post-translationally added hydroxyl group.
-!- MISCELLANEOUS: The complete chain contains 1052 residues.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        6; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TISSUE=Kidney;
MabLine=24266642; PubMed=8206952;
Nab H.-D., Niu Z., Adams S.L.;
"An alternative transcript of the chick type III collagen gene that does not encode type III collagen.";
J. Biol. Chem. 269:16443-16448 (1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 1; Length 779;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pred. No. 5.8e-33;
4; Mismatches 50; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (POTENTIAL).
(POTENTIAL).
(POTENTIAL).
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HYDROXYLATION (POTENTIAL)
HYDROXYLATION (POTENTIAL)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    208
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    175 GLPGPAGPPGEAGKPGEQGVPGDLGAPGPSGPAG
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HYDROXYLATION
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70346 MW;
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nes 154; Conservative
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779 AA;
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CA13 CHICK
ID CA13 CH
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DT 01-0CT
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DE COLLAG
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52 GSPGEAGRPGEAGLPGAKGLTGSPGSPGPDGKTGPPGPAGQDGRPGPPGPPGARGQAGVM 111
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SEQUENCE OF 1227-1496 FROM N.A.
MEDLINE-65289337; PubMed=2411731;
MFDLINE-65289337; PubMed=2411731;
MYORE J.C., Loidl H.R., Seyer J.M., Dion A.S.;
"Complete primary structure of the human alpha 2 type V procollagen COOH-terminal propeptide.";
J. Biol. Chem. 260:11216-11222(1985).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE OF 398-1496 FROM N.A.
MEDLINE-87146331; PubMed=3029669;
Weil D., Bernard M.P., Gargano S., Ramirez F.;
The pro alpha 2(V) collagen gene is evolutionarily related to the major fibrillar-forming collagens.";
Nucleic Acids Res. 15:181-198(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Woodbury D., Benson-Chanda V., Ramirez F.; Modbury D., Benson-Chanda V., Ramirez F.; Manino-Cerminal propeptide of human pro-alpha 2(V) collagen conforto the structural criteria of a fibrillar procollagen molecule."; J. Biol. Chem. 264:2735-2738(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE OF 1449-1496 FROM N.A.
MEDLINE-89138450; PubMed=3224983;
Tsipouras P., Schwartz R.C., Liddell A.C., Salkeld C.S., Weil D.,
Ramirez F.;
                                                                                       .) (POTENTIAL)
995 INTERCHAIN (BY SIMILARITY).
262 HYDROXYLATION (BY SIMILARITY).
263 HYDROXYLATION (BY SIMILARITY).
859 HYDROXYLATION (BY SIMILARITY).
1163 N-LINKED (GLONAC. .) (POTENTIAL
96 E - K (IN REF. 2).
1132 F -> S (IN REF. 3).
AA; 121249 MW; 96ABE7B2E9DEB43D CRC64;
                                                                                                                                                                                              Length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               638 GLÓGLÞGGPGPAGENGKPGEPGPKGDIGGPGFPGPKG 674
                                                                                                                                                                                              67.1%; Score 794.5; DB 1;
65.9%; Pred. No. 2e-31;
ive 13; Mismatches 52;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       172 GFQGLPGPAGPPGEAGKPGEQGVPGDLGAPGPSGPAG
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01-07N-1990 (Rel. 13, Last sequence update)
01-0CT-2003 (Rel. 42, Last annotation update)
collagen alpha 2(V) chain precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT; 1496 AA
                                                                                                                                                                                                                                        143; Conservative
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        Homo sapiens (Human)
                                                                                                                                                                                                                      Similarity
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P05997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
                                                                                                                                                                                                                                                                                 Nucleic Acids Res. 11:2733-2744(1983).

Nucleic Acids Res. 11:2733-2744(1983).

-!- FUNCTION: Collagen type III occurs in most soft connective tissues along with type I collagen.

-!- SUBBUIT Trimers of indentical alpha 1(III) chains. The chains are linked to each other by interchain disulfide bonds. Trimers are also cross-linked via hydroxylysines.

-!- FUNT Prolines at the third position of the tripeptide repeating unit (G-X-Y) are hydroxylated in some or all of the chains.
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TRIPLE-HELICAL REGION (BY SIMILARITY).
NONHELICAL REGION (C-TERMINAL) (BY
           SEQUENCE OF 29-96; 332-397; 431-484; 503-535 AND 869-976 FROM N.A. BEDLINES-84270656; PubMed-e547770; Yanada Y., Liau G., Mudryj M., Obici S., de Crombrugghe B.; "Conservation of the sizes for one but not another class of exons
                                                                                                                                                          SEQUENCE OF 977-1262 FROM N.A.
MEDLINE=83220816; PubMed=6856474;
Yamada Y., Kuhn K., de Crombrughe B.;
"A conserved nuclecide sequence, coding for a segment of the C-
propeptide, is found at the same location in different collagen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NONHELICAL REGION (N-TERMINAL) (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PROSITE; PSO1208; VWFC 1; 1.
PROSITE; PSS0184; VWFC 2; 1.
Extracellular matrix; Connective tissue; Repeat; Hydroxylation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              POTENTIAL.
AMINO-TERMINAL PROPEPTIDE (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COLLAGEN ALPHA 1 (III) CHAIN.
CARBOXYL-TERMINAL PROPEPTIDE
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InterPro; IPR008160; Collagen.
InterPro; IPR00160; Fib_collagen.C.
InterPro; IPR001011; Fibrinogen.C.
InterPro; IPR001007; VWF.C.
ProDom; PD000007; Clg helix; 1.
ProDom; P0002078; Fib_collagen.C; 1.
SYART; SW00214; VWC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      X00822; CAB52686.1;
X00823; CAB52686.1; JOINED.
X00825; CAA55397.1; ALT SEQ.
X00825; CAA55399.1; JOINED.
X00827; CAA55399.1;
X00828; CAA55399.1;
X00830; CAA5401.1;
X00831; CAA5401.1;
X00831; CAA5401.1;
X00831; CAA5401.1;
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M36662; AAA18519.1; ALT_SEQ.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; U07973; AAA83407.1; -.
                                                                                           two chick collagen genes.";
Nature 310:333-337(1984).
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164
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PIR; I50694; I50694
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145
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SIGNAL
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SEQUENCE OF 208-227.

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                                                                                                                                                                                                                                                                                                                                                              "A single base mutation in COL5A2 causes Ehlers-Danlos syndrome type II.",
                                                                                                                                                                                                                                            Michalickova K., Susic M., Willing M.C., Wenstrup R.J., Cole W.G., "Mutations of the alpha2(V) chain of type V collagen impair matrix assembly and produce Ehlers-Danlos syndrome type I."; Hum. Mol. Genet. 7:249-255(1998).
                                                                                                                                                                                                                                                                                                                       MEDLINE=98455031; PubMed=9783710;
Pichards A.J., Martin S., Nicholls A.C., Harrison J.B., Pope F.M.,
                                                                                                             TISSUE=Bone;
MEDLINE=94237164; PubMed=8181482;
Moradi-Ameli M., Rousseau J.C., Kleman J.P., Champliaud M.F.,
Boutillon M.M., Bernillon J., Wallach J.M., van der Rest M.;
"Diversity in the processing events at the N-terminus of type-V
                                                 Isolation of the alpha 3-chain of human type V collagen and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MIM; 130010; -.
GO; GO:0005588; C:collagen type V; TAS.
GO; GO:0008151; P:cell growth and/or maintenance; TAS.
InterPro; IPR008161; Clg helix.
InterPro; IPR008160; Collagen.
InterPro; IPR008885; Fib_collagen_C.
                                                              characterization by partial sequencing."
Biol. Chem. Hoppe-Seyler 373:69-75(1992)
                                                                                                                                                                                            Eur. J. Biochem. 221:987-995(1994),
            TISSUE=Placenta;
MEDLINE=92239022; PubMed=1571108;
                                                                                                                                                                                                                                MEDLINE=98087576; PubMed=9425231;
                                                                                                   SEQUENCE OF 288-297 AND 606-617.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; J04478; AAA51859.1; -.
EMBL; X04758; CAA28454.1; -.
EMBL; M11718; AAA52058.1; -.
PIR; A31427; CGHUZV.
PDB; 1A9A; 18-NOV-98.
Genew; HGNC:2210; COL5A2.
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                                                                                                                                                                               collagen.
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61 GEAGLPGAKGLTGSPGSPGPDGKTGPPGPAGQDGRPGPPGPPGARGQAGVMGFPGPKGAA 120
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Mammalia; Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                          Probom, Provided to the property of the proper
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CARBOXYL-TERMINAL PROPEPTIDE.
VWPC.
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MEDLINE=89350838; PubMed=2764886;
Ala-Kokko L., Kontusaari S., Baldwin C.T., Kuivaniemi H.,
Prockop D.J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                960 960 G-> R (in EDS-II).
22 292 A - P (IN REF. 6).
1418 1418 K -> T (IN REF. 3).
1450 1460 E -> O (IN REF. 3).
1460 1460 V -> A (IN REF. 3).
1496 AA, 144720 MW, 82827CI7A8644F5A CRC64;
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01-JRN-1990 (Rel. 13, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Collagen alpha 1(III) chain precursor.
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HYDROXYLATION.
G -> R (in EDS
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InterPro, IPR002181; Fibrinogen_C.
InterPro, IPR001007; VWF_C.
Edm, PF01410, COLF1; 1.
Pfam; PF01391; Collagen; 18.
Pfam; PF00093; vwc; 1.
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Prockop D.J.; "Structure of cDNA clones coding for the entire prepro alpha 1 (III)

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VARIANT SEQUENCE OF 1176-1466 FROM N.A.
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MEDLINE=93293988; PubMed=8514866;
Tromp G., Wu Y., Prockop D.J., Madhatheri S.L., Kleinert C.,
Earley J.J., Zhuang J., Noerrgaard O., Darling R.C., Abbott W.M.,
Cole C.W., Jaakkola P., Ryynaenen M., Pearce W.H., Yao J.S.T.,
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the alpha 1 (III) chain of type III procollagen exposes an arginine
and causes Ehlers-Danlos syndrome IV.";
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TISSUB=Placenta;
MEDLINE=88303360; PubMed=3405773;
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ONDER OF CNDR PEPTIDES.

MEDLINE=70181852; PubMed=5443712;

MEDLINE=70181852; PubMed=5443712;

Wust J., Lane J.M., Fletzek P.P., Miller E.J., Piez K.A.;

"The order of the CNBr peptides from the alpha 2 chain of collagen.";

Biochem. Biophys. Res. Commun. 38-703-708 (1970).

-! FUNCTION: Type I collagen is a member of group I collagen

(fibrillar forming collagen).

-!- SUBUNT: Trimers of one alpha 2(I) and two alpha 1(I) chains.

-!- SUBUNT: Trimers of one alpha 2(I) and two alpha 1(I) chains.

-!- TISSUE SPECIFICITY: Forms the fibrils of tendon, ligaments and bones. In bones the fibrils are mineralized with calcium
                                                                                                                                                                                                                                                                                                        Fietzek P.P., Piez K.A.; "Isolation of the cyanogen bromide peptides from "Isolation and characterization of the cyanogen bromide 2 chain of rat skin collagen."; Blochemistry 8:2129-2133(1969).
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"The covalent structure of collagen: amino acid sequence of the N-terminal region of alpha2-CB3 from rat skin collagen and alpha2-CB3.5 from calf skin collagen.";
                                                                                        TISSUE=Skin;
MEDLINE=67162268; PubMed=5337886;
Kang A.H., Bornstein P., Piez K.A.;
"The amino acid sequence of peptides from the cross-linking region
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-!- PTM: Prolines at the third position of the tripeptide repeating unit (G-X-Y) are hydroxylated in some or all of the chains.
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Fietzek P.P., Kell I., Kuehn K.;
The covalent structure of collagen. Amino acid sequence of the N-
terminal region of alpha 2-CB4 from calf and rat skin collagen.";
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peptides from chick and rat skin collagens.";
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Submitted (JAN-1999) to the EMBL/GenBank/DDBJ databases.
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MEDLINE=74055004; PubMed=4763308;
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TISSUE=Skin;
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                                                                                                                                                                                                                                                                                                                                                            MEDLINE=90037070; PubMed=2808425;
Tromp G., Kuivaniemi H., Stolle C.A., Pope F.M., Prockop D.J.;
"Single base mutation in the type III procollagen gene that converts
the codon for glycine 883 assartate in a mild variant of
Ehlers-Danlos syndrome IV.";
                                                                                                                                                                                                             "A single base mutation in the gene for type III collagen (COL3A1) converts glycine 847 to glutamic acid in a family with Ehlers-Danlos syndrome type IV. An unaffected family member is mosaic for the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Rattus norvegious (Rat).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Rattus.
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in a
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Richards A.J., Ward P.N., Narcisi P., Nicholls A.C., Lloyd J.C.,
                      Madhatheri S.L., Kuivaniemi
793 in type III procollagen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Characterisation of a glycine to valine substitution at amino position 910 of the triple helical region of type III collagen patient with Ehlers-Danlos syndrome type IV."; J. Med. Genet. 28:458-463(1991).
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Richards A.J., Lloyd J.C., Ward P.N., de Paepe A., Narcisi P.,
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Johnson P.H., Richards A.J., Pope F.M., Hopkinson D.A.;
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P02466; Q9RIEB;
21-JUL-1986 (Rel. 01, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
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                    Tromp G., de Paepe A., Nuytinck I.,
"Substitution of valine for glydine
Ehlers-Danlos syndrome type IV.";
Hum. Mutat. 5:179-181(1995).
MEDLINE=95268429; PubMed=7749417;
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VARIANT EDS-IV ASP-1050.
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388 GSPGEPGSAGPAGPPGLRGSPGSRGLPGADGRAGVMGPPGNRGSTGPAGVRGPNGDAGRP 447
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
                                                                                                                                                                                                               Extracellular matrix; Connective tissue; Repeat; Hydroxylation; Glycoprotein; Collagen; Signal; Pyrrolidone carboxylic acid. SIGNAL 1 POTENTIAL. PROPEP 25 AMINO-TERMINAL PROPEPTIDE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          568 GTAGEVGKPGERGLPGEFGLPGPRG 595
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              181 GPPGEAGKPGEQGVPGDLGAPGPSGPAG 208
           EMBL, AF121217; AAD41775.1; -.
InterPro; IPR008161; Clg helix.
InterPro; IPR008160; Collagen.
InterPro; IPR000885; Fib_collagen_C.
Pfam; PF01410; COLFI; 1.
ProDom; PD000007; Clg_helix; 4.
ProDom; PD002078; Fib_collagen_C; RACDENCEN; SMART; SM0038; COLFI; 1.
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STRAIN-C57BL/6 X DBA; TISSUE-Embryo;
MEDLINE-95011609; PubMed-7926795;
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Matches 139; Conserv
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A REDLINE=22388257; PubMed=12477932;
A KITALNE=20.7548257; PubMed=12477932;
A REDLINE=22388257; PubMed=12477932;
A Altschul S.F., Zeeberg B., Wagner L., Shamen C.R., Schuler G.D.,
A Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
A Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
A Stapleton M. Scares M.B., Bonaldo M.F., Clasavant T.L., Scheetz T.E.,
Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
A Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.T.,
B Rosak S.A., McEnan P.J., McKernan K.J., Lu X., Gibbs R.A.,
A Nilalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,
Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Blakesley R.W., Touchman M., Gren E.D., Dickson M.C.,
Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
Generation and initial analysis of more than 15,000 full-length
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
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CONTRAINSCRIBLOGIT TISSUB-Embryonic head;

MEDLINE-21085660; PubMed=11217851;

Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,

A Arakawa T., Hara A., Pukunishi Y., Konno H., Adachi J., Fukuda S.,

A Arakawa T., Hara A., Pukunishi Y., Konno H., Adachi J., Yamanaka I.,

A Arawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,

A Radora K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,

Kadora K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,

Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,

Kuchi P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,

Kuchi P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,

Kuchi P., Lewis S., Batuli F., Suzuki R., Tomita M., Wagner L., Washio T.,

Blake J., Boficali D., Bojunga N., Carninci P., de Bonaldo M.F.,

Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,

Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,

Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,

Nordone P., Ring B., Ringwald M., Rodriguez I., Sakameto N.,

Sasaki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,

M. Wonshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                N-terminal domains of the murine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDINE-85131189; PubMed=3972847;
Liau G., Mudryj M., de Crombrugghe B.;
"Identification of the promoter and first exon of the mouse alpha 1
          "The mouse type-III procollagen-encoding gene: genomic cloning and complete DNA sequence.";
Gene 147:161-168(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hayashizaki Y.; "Functionation of a full-length mouse cDNA collection."; Nature 409:685-690(2001).
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Metsaeranta M., Toman D., de Crombrugghe B., Vuorio E.;
"Specific hybridization probes for mouse type I, II, III and IX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE OF 1-488 FROM N.A.
MEDLINE=88167858; PubMed=3443309;
Wood L., Theriault N., Vogeli G.;
"Complete nucleotide sequence of the langhal type-III collagen chain.";
Gene 61:225-230(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         II) collagen gene.";
Biol. Chem. 260:3773-3777(1985).
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STRAIN=C57BL/6; TISSUE=Brain;
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61 GEAGLPGAKGLTGSPGSPGPDGKTGPPGPAGQDGRPGPPGPPGPRGQAGVMGFPGPKGAA 120
                                                                                                           121 GEPGKAGERGVPGPPGAVGPAGKDGEAGAQGPPGPAGPAGERGEQGPAGSPGFQGLPGPA 180
                                                                 527 GTPGGPGIRGMPGSPGGPGNDGKPGPPGSQGESGRPGPPGPSGPRGQPGVMGFPGPKGND
                                                                                                                                                                                                                                                                                                                                         STANDARD;
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SEQUENCE OF 1-242.
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Biochim. Biophys, Acta 1089:241-243(1991).
-!- FUNCTION: Collagen type III occurs in most soft connective tissues along with type I collagen.
-!- SUBUNIT: Trimers of identical alpha 1(III) chains. The chains are
                                                                                                                                                                                             to
(By
                                                             SUBUNIT: Trimers of identical alpha 1(III) chains. The chains are linked to each other by interchain disulfide bonds. Trimers are also cross-linked via hydroxylysines.
PTM: Proline residues at the third position of the tripeptide repeating unit (G-X-Y) are hydroxylated in some or all of the
                                                                                                                                                                                    PIM: O-linked glycan consists of a Glc-Gal disaccharide bound to the oxygen atom of a post-translationally added hydroxyl group
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R EMBL; AX019449; BAB31724.1; -
R EMBL; AX019449; BAB31724.1; -
R EMBL; AX019449; BAB31724.1; -
R EMBL; X57983; CATA1048.1; -
R PIR; S5986; S5986;
R MGD; MGI: 88453; CG13a1.
R InterPro; IPR001861; Cl1g helix.
R InterPro; IPR001865; Fib_collagen_C.
R InterPro; IPR001865; Fib_collagen_C.
R InterPro; IPR001865; Fib_collagen_C.
R Pfam; PF01391; Collagen; 18.
R Probom; PD010007; C1g helix; 1.
R Probom; PD010007; C1g helix; 1.
R Probom; PD010018; Fib_collagen_C; 1.
R MART; SM0018; COLFI; 1.
R SMART; SM0018; VWC; 1.
R PROSITE; PS01208; VWFC_1; 1.
R PROSITE; PS01208; VWFC_2; 1.
R PROSITE; PS01208; VWFC_2; 1.
R EXTERCEPLUAL matrix; Connective tissue; Repeat; Hydroxylation;
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59 NONHELICAL REGION (N-TERMINAL).
64 NONHELICAL REGION (C-TERMINAL).
65 NONHELICAL REGION (C-TERMINAL).
65 NONHELICAL REGION (C-TERMINAL).
62 HYDROXYLATION (BY SIMILARITY).
63 HYDROXYLATION (BY SIMILARITY).
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65 HYDROXYLATION (BY SIMILARITY).
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67 HYDROXYLATION (BY SIMILARITY).
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COLLAGEN ALPHA 1(III) CHAIN.
CARBOXYL-TERMINAL PROPEPTIDE.
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Pred. No. 6.7e-30;
13; Mismatches 59;
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                                                                                                                                                                                                                                similarity).
SIMILARITY: Contains 1 VWFC domain.
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MEDINE=80026027; PubMed=488907;
Dewes H., Fietzek P.P., Kuhn K.;
"The covalent structure of calf skin type III collagen. II. The amino acid sequence of the cyanogen bromide peptide alpha 1(III)CB1,8,10,2 (positions 223-402).";
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chain
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MEDLINE-80026030; Pubmed-488910;
Dewes H., Fietzek P.P., Kuhn K.;
The covalent structure of calf skin type III collagen. V. The amino acid sequence of the cyanogen bromide peptide alpha 1(III)CB9A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE OF 423-571.

MEDLINE-80026028; PubMed=488908;
Bencz H., Fietzek P.P., Kuhn K.;
"The covalent structure of calf skin type III collagen. III. The amino acid sequence of the cyanogen bromide peptide alpha I(III)CB4 (positions 403-551).";
                                                                                                                                                                                                                                                                                                                   Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, amamalia, Eutheria, Cetartiodactyla, Ruminantia, Pecora, Bovoldea, Bovidae, Bovinae, Bos.

NCBI_TaxID=9913;
                                                                                                                                                                                                                                                                                                                                                                                                                                       Fietzek P.P., Allmann H., Rauterberg J., Henkel W., Wachter B.,
Kuhn K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "The covalent structure of calf skin type III collagen. I. The acid sequence of the amino terminal region of the alpha 1(III)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE-80026029; PubMed-488909;
Lang H., Glanville R.W., Fietzek P.P., Kuhn K.;
"The covalent structure of calf skin type III collagen. IV. Th
acid sequence of the cyanogen bromide peptide alpha 1(III)CBS
(positions 552-788).";
Hoppe-Seyler's Z. Physiol. Chem. 360:841-850(1979).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hoppe-Seyler's Z. Physiol. Chem. 360:821-832(1979)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hoppe-Seyler's Z. Physiol. Chem. 360:833-840(1979)
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MEDLINE-80026031; PubMed-488911;
Allmann H., Fietzek P.P., Glanville R.W., Kuhn K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (position 789-927).";
Hoppe-Seyler's Z. Physiol. Chem. 360:851-860(1979)
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                                             181 GPPGEAGKPGEQGVPGDLGAPGPSGPAG 208
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20-MAR-1987 (Rel. 04, Last seq
16-OCT-2010 (Rel. 40, Last ann
Collagen alpha 1(III) chain.
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467 GSPGEPGANGLPGAAGERGPSGFRGPAGPNGIPGEKGPPGERGGPGPAGPRGVAGEPGRD 526 GPPGEPGPTGLPGPPGERGGPGSRGFPGADGVAGPKGPAGERGSPGPAGPKGSPGEAGRP 60

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61 GEAGLPGAKGLTGSPGSPGPDGKTGPPGPAGQDGRPGPPGPPGARGQAGVMGFPGPKGAA 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   372 GLPGGPGLRGIPGSPGGPGSNGKPGPPGSQGETGRPGPPGSPGPRGQPRGPPFKGND 431
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                121 GEPGKAGERGVPGPPGAVGPAGKDGEAGAQGPPGPAGPAGERGEQGPAGSPGFQGLPGPA 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  432 GAPGKNGERGGPGGPGPPGPPGFNGETGPQGPPGPPGPSGDKGDTGPPGPQGLQGLPGTS 491
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 GPPGEPGPTGLPGPPGERGGPGSRGFPGADGVAGPKGPAGERGSPGPAGPKGSPGEAGRP 60
Gaps
                                                                                                                                                                                                           Interpro; IPR008161; Clg_helix.
Interpro; IPR008160; Collagen.
Interpro; IPR001007; VWF C.
Pfam; PF01391; Collagen, 17.
Prodom; PD000007; Clg_helix; 3.
PR051TE; PS01208; VWFC_1; PARTIAL.
Extracellular matrix; Connective tissue; Repeat; Hydroxylation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          21;
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Best Local Similarity 60.4%; Pred. No. 6.3e-30;
Matches 139; Conservative 15; Mismatches 55; Indels 21;
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TRIPLE-HELICAL REGION.
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Search completed: September 24, 2004, 11:07:23 Job time : 7.27357 secs

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Compugen Ltd.
GenCore version (c) 1993 - 2004
          Copyright
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sw model - protein search, using OM protein 6 ; Search time 8.04914 Seconds (without alignments) 2497.663 Million cell updates/sec September 24, 2004, 11:06:56 Run on:

US-10.658-989A-1 1184 1 GPPGEPGPTGLPGEPGERGG......GEQGVPGDLGAPGPSGPAGG 209 Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283366 segs, 96191526 residues Searched:

283366 of hits satisfying chosen parameters: Total number

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

summaries Post-processing: Minimum Match 0% Maximum Match 100 Listing first 45

PIR_78:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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Copecies: Homo sapiens (man)
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Copecies: Homo sapiens
Condition
Complete national soluta; Agains; ISS254; A39943; ISS237; A35233; S09400; B90567; S11:
S269; A29499; IS3466; A02682; I37247
R;D'Alessio, M.; Bernard, M.; Pretorius, P.J.; de Wet, W.; Ramirez, F.; Pretorious, P.J.
Gene 67, 105-114, MUD:89329734; PMID:2843432
A,Accession: I60114; MUID:89329734; PMID:2843432
A,Accession: Gondled from GB/EMBL/DDBJ
A,Accession: Gondled from GB/EMBL/DDBJ
A,Accession: GB:MZ0789; NID:9179593; PIDN:AAB59373.1; PID:9179594
A,Accession: GB:MZ0789; NID:9179593; PIDN:AAB59373.1; PID:9179594
A,Accession: GB:MZ0789; NID:9179593; PIDN:AAB59373.1; PID:9179594
A,Accession: S01143
A,Accession: M.; Astala A,Accession: M.; Myers, J.; J3-JUN-1988
A,CCCSS-references: EMBL:X07884; NID:930015; PIDN:CAA30731.1; PID:930016; GB:M36546; NID
A,RESTOR COMPLETED A,CCCSS-REFERENCES: EMBL-GanBank/DDBJ databases by Prockcy, D.J., 13-JUN-1988
A,Accession: S01143
A,Accession: S01143
A,Accession: S01143; MUD:930015; PIDN:CAA30731.1; PID:930016; GB:M36546; NID
A,RETER Human proalpha1(1) collagen gene structure reveals evolutionary conservation of A,Reference number: A93335; MUD:84270697; PMID:6462220
A,Recession: A,Accession number: A93335; MUD:84270697; PMID:6462220
A,Accession: A,Accession number: And A,Accession number: Adams A,Accession number: Adams A,Accession number: Adams A,Accession number: A,Accession number: Adams A,Accessi

A, Molecule type: DNA A, Residues: 1-58, 'Q', 60-181 «CHU> A, Croos-sternces: 1-58, 'Q', 60-181 «CHU> A, Croos-sternces: EMBL: X00820; NID: 935657; PIDN: CAA25394.1; PID: 935658 B, Rossouw, C.M.S.; Vergeer, W.P.; du Plooy, S.J.; Bernard, M.P.; Ramirez, F.; de Wet, W.L. J. Biol. Chem. 262, 15151-15157, 1987 A; Title: DNA sequences in the first intron of the human pro-alpha 1(I) collagen gene enh? A; Reference number: 155254; MUID: 88033098; PMID: 222714 A; Accession: 155254

A;Status: translation not shown; translated from GB/EMBL/DDBJ
A;Residues: translation not shown; translated from GB/EMBL/DDBJ
A;Residues: 1-45 cROS>
A;Cross-references: GB:072829; NID:9180387; PIDN:AAAS1993.1; PID:9180388
B;Bornstein, P; McKay, J; Morishima, J.K.; Devarayalu, S.; Gelinas, R.E.
Proc. Natl. Acad. Sci. U.S.A. 84, 8869-8873, 1987
A;Title: Regulatory elements in the first intron contribute to transcriptional control of A;Reference number: A39943; MUID:88097389; PMID:3480516

A;Molecule type: DNA A;Residues: 1.34 kBOR> A;Cross-references: GB.J03559; NID:g180876; PIDN:AAA52052.1; PID:g553238 R;Chu, M.L.; de Wet, W.; Bernard, M.; Ramirez, F.

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A; Molecule type: mRNA A; Molecule type: Molecule
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A; Residues: 710-720, 'E',722-737,'E',739-745 < WAL>
A; Residues: 710-720, 'E',722-737,'E',739-745 < WAL>
A; Note: the authors translated the codons CAG for 721 and CGT for 738 as Glu
R; Forlino, A.; Zolezzi, F.; Valli, M.; Pignatti, P.F.; Cetta, G.; Brunelli, P.C.; Mottes,
Hum. Mol. Genet. 3, 2201-2206, 1994
A; Title: Severe (type III) osteogenesis imperfecta due to glycine substitutions in the ce
A; Reference number: I54365; MUID:95187161; PMID:7881420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Molecule type: DNA
A; Residues: 746-766,'S',768-781 <FOR>
A; Residues: 746-766,'S',768-781 <FOR>
A; Rossidues: 746-766,'S',768-781 <FOR>
A; Cross-references: GB:L47667; NID:g1009093; PIDN:AABS9576.1; PID:g1009094
B; Chessler, S.D.; Wallis, G.A.; Pyrs, P.H.
J. Biol. Chem. 268, 18218-18225, 1993
A; Title: Mutations in the carboxyl-terminal propeptide of the pro alpha 1(I) chain of tyr
A; Reference number: A47426; MUID:93352646; PMID:8349697
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A;Residues: 1179-1276,'H',1278-1336,1339-1387,'R',1389-1464 CHE>
A;Cross-references: GB:S64596; NID:g407589; PIDN:AB27856.1; PID:g407590
A;Note: sequence extracted from NCBI backbone (NCBIN:136444, NCBIP:136445)
A;Note: does not represent an experimentally determined sequence but three different muta
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R; Cohn, D.H.; Apone, S.; Eyre, D.R.; Starman, B.J.; Andreassen, P.; Charbonneau, H.; Nick, D. Biol. Chem. 263, 14605-14607, 1988
A; Title: Substitution of Cysteine for Glycine within the Carboxyl-terminal Telopeptide of A; Reference number: 155269; WUID: 89008319; PMID: 3170557
A; Accession: 155269
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A,Title: Nucleotide sequences of complementary deoxyribonucleic acids for the proalphal A,Reference number: A90476; MUID:84080385; PMID:6689127 A,Accession: A90476
A;Accession: I52905
A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Residues: 342-352, ~C',354-359 <WI2>
A;Cross-references: GB:S64717; NID:g408195; PIDN:AAB27677.1; PID:g408196
A;Cross-references: GE:S64717; NID:g408195; PIDN:AAB27677.1; PID:g408196
B;Note: mutant sequence from partient with osteogenesis imperfecta
B;Bernard, MP.; Chu, M.L.; Myers, J.C.; Ramirez, F.; Eikenberry, E.F.; Prockop, Biochemistry, 22, 5213-5223, 1993
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Residues: 1179-1387,'R',1389-1464 <CH7>
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A,Residues: 1179-1276,'H',1278-1464 <CH5>
A,Experimental source: fetal cell 86-237
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Experimental source: fetal cell 86-146
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A; Residues: 1179-1464 < CH4>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               A,Cross-references: GB:M10627; NID:g180383; PIDN:AAA51992.1; PID:g553226
KWHILE, M.K.; Keene, D.R.; HOLT, H.; Glanville, R.W.; Steinmann, B.; Rao, V.H.; Hollist
J. Biol. Chem. 265, 6312-6317, 1990
A,Title: In vivo and in vitro noncovalent association of excised alpha1(I) amino-termina
Tome, type VII.
A;Reference number: A35233; MUID:90202908; PMID:2318855
A;Accession: A35233
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Residues: 156-183 <MEI>
Residues: 156-183 <MEI>
Lochemistry 9, 4699-4706, 1970

Jittle: Isolatrion and characterization of the cyanogen bromide peptides from the alphal Reference number: A90867; MUID:11038625; PMID:5529814
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A; Molecule type: protein

A; Molecule type: protein

A; Nesiduces: 175-187; 214-287, 'P', 289 cBAB>

A; Note: sequence of collagen alpha 1(S)(I) isolated from bone after pepsin digestion

B; Deak, S.B.; Scholz, P.M.; Amenta, P.S.; Constantinou, C.D.; Levi-Minzi, S.A.; Gonzalez

J; Biol. Chem. 266, 21827-21832, 1991

A; Title: The substitution of arginine for glycine 85 of the alpha 1(I) procollagen chain ooperative melting of intact type I collagen.

A; Reference number: 155342; MUID:92042092; PMID:1718984
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A;Molecule type: mRNA
A;Note: sequences from the 5' and 3' ends only are shown; mutant sequence 263-Arg report
A;Molecule type: MG, Segrest, J.P.; Cunningham, L.W.
A;Molecule type: MRNA
A;Molecule type: 
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A; Realduse: 33-26 wIRs
A; Residuse: 33-26 wIRs
A; Note: this propeptide fragment remained non-covalently bound to a defective, uncleaved
B; Mote: this propeptide fragment remained non-covalently bound to a defective, uncleaved
B; Weil, D; d'Alessio, M; Ramirez, F; de Wet, W; Cole, W.G.; Chan, D.; Bateman, J.F.
EMBO J. 8, 1706-1710, 1999
A; Title: A base substitution in the exon of a collagen gene causes alternative splicing
A; Title: A base substitution in the exon of a collagen gene causes alternative splicing
A; Reference number: S09400; MUID:89356643; PMID:2767050
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A;Residues: 281-302;402-420;823-843;925-944;1026-1045;1143-1162 <LAB>
A;Residues: 281-302;402-420;823-843;925-944;1026-1045;1143-1162 <LAB>
R;Wirtz, M.K.; Rao, V.H.; Glanville, R.W.; Labhard, M.E.; Pretorius, P.J.; de Vries, W.N.
Connect. Tissue Res. 29, 1-11, 1993
A;Title: A cysteine for glycine substitution at position 175 in an alpha 1 (I) chain of
A;Reference number: I52905; MUID:93339642; PMID:8339541
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A;Recession: A92069
A;Molecule type: protein
A;Residues: 263-268 <MOR>
A;Residues: 263-268 <MOR>
      Biol. Chem. 260, 2315-2320, 1985
Title: Fine structural analysis of the human pro-alpha 1 (1) collagen gene. Promoter Keference number: 155237; MUID:85130970; PMID:2857713
Accession: 155237
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Matrix 10, 124-130, 1990
A;Title: Segmental amplification of the entire helical and telopeptide regions of the A;Reference number: S15989; MUID:90326017; PMID:2374517
A;Accession: S15989
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A;Note: attachment of 2-O-alpha-D-glucosyl-O-beta-D-galactose to 5-hydroxylysine
                                                                                                                                                A;Reference number: 155237; MÜID:85130970; PMID:2857713
A;Accession: 155237
A;Status: translation not shown; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
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Residues: 1-34 <CH2>
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,Molecule type: protein
,Residues: 140-238 «BAL»
,Residues: 140-238 «BAL»
,Baljan, G.; Click, E.M.; Hermodson, M.A.; Bornstein, P.
ijochemistry 11, 3798-3806, 1972
,Title: Structure of rat skin collagen alphal-CB8. Amino acid sequence of the hydroxylar
,Reference number: A90362; MUID:73006942; PMID:4342027
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',Residues: 339-418 cBA2>
',Residues: 339-418 cBA2>
',Experimental source: skin
';Butler, W.T.; Underwood, S.P.; Finch Jr., J.E.
'iooflemistry 13, 2946-2953, 1974
',Title: Chemical studies on the cyanogen bromide peptides of rat skin collagen. Amino a'
',Title: Chemical studies on the cyanogen bromide peptides of rat skin collagen. Amino a'
',Teterence number: A90379; MUID:74271984; PMID:4366532
'Contents: CNB-3
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Bur. J. Blochem. 37, 287-294, 1973
A;Title: Structural and immunogenic properties of a major antigenic determinant in neutr.
A;Reference number: A91209; MUID:74011954; PMID:4126850
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ESES Lett. 26, 61-65, 1972
A;Itle: Non-helical regions in rat collagen alphal-chain.
A;Reference number: A91385; MUID:73049495; PMID:4636751
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A. Molecule type: protein
A. Molecule type: protein
A. Molecule type: protein
A. Roberimental source: skin
B. Balian, G.; Click, E.M.; Bornstein, P.
Biochemistry 10, 4470-4478, 1971
B. Structure of rat skin collagen alphal-CB8. Amino acid sequence of the hydroxylar
A. Reference number: A90357; MUID:72136131; PMID:4335087
A. Contents: CNBT8
                                                                                              rat skin collagen. The cov
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Pred. No. 1.9e-55;
                                             Biochemistry 9, 44-50, 1970

A;Title: Chemical studies on the cyanogen bromide peptides of A;Reference number: A90566; MUID:70085124; PMID:5411206

A;Contents: CNBr5
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A;Residues: 419-567 <BU3>
A;Experimental source: skin
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A, Residues: 568-651 <ST1>
A, Experimental source: skin
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1, Residues: 651-671 <ST2>
1, Experimental source: skin
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Collagen alpha 1(1) chain - rat (tentative sequence) (fragments)

Collagen alpha 1(1) chain - rat (tentative sequence)

Collagen alpha 1(2) chain - rat (tentative sequence)

Collagen alpha 1(3) chain - rat (tentative sequence)

Collagen alpha 1(3) chain - rat (tentative sequence)

Collagen alpha 1(3) chain - rat (tentative sequence)

Recomparative sequence revision 13-01-1881

Recomparative sequence studies of rat skin and tendon collagen. II. The absence chain the rate of the rate o
                                                                                                                                                                                                                                           for the C-propeptide domain.
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A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1187-1194, 'C',1196-1220 <COH>
A;Corsa-references: GB:N23213; NID:g340842; PIDN:AABS9363.1; PID:g499622
A;Note: mutant sequence from a patient with mild osteogenesis imperfecta
A;Note: mutant sequence from a patient with mild osteogenesis imperfecta
Nucleic Acids Res. 16, 349, 1988
A;Title: Human pro-alpha-1(I) collagen: cDNA sequence for the C-propeptio
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A,Molecule type: mRNA
A,Molecule type: mRNA
A,Kossudes: 518-1128 <FRE>
A,Cross-references: GB:N14423; NID:g192261; PIDN:AAA37333.1; PID:g192262
A,Cross-references: GB:N14423; NID:g192261; PIDN:AAA37333.1; PID:g192262
B;Monson, J.M.; Friedman, J.; McCarthy, B.J.
A,Mol. Cell. Biol. 2, 1362-1371, 1982
A,Fitle: DNA sequence analysis of a mouse pro-alpha-1(I) procollagen gene: Evidence for A,Reference number: 149559; MUID:83141374; PMID:6298597
A,Accession: 149559
A,Accession: I49559
A,Accession: preliminary; translated from GB/EMBL/DDBJ
A,Residues: 735-1130 <RES>
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A; Residues: 1-1453 - L153
B; Metsaeranta, M.; Toman, D.; de Crombrugghe, B.; Vuorio, E.
B; Metsaeranta, M.; Toman, D.; de Crombrugghe, B.; Vuorio, E.
B; Crombra, B; Dypy, 2.41-243, 1991
A; Title: Specific hybridization probes for mouse type!, II, III and IX collagen mRNAs A; Reference number: S16176; MUID:91274355; PMID:2054384
A; Astatus: preliminary
A; Astatus: preliminary
A; Astatus: preliminary
A; References: EMB::X57981; NID:950484; PIDN:CAA41046.1; PID:950485
A; Rerench, B.T.; Lee, W.H.; Maul, G.G.
Gene 3) 311-312, 1985
A; Title: Nucleotide sequence of a cDNA clone for mouse proalphal(I) collagen protein.
A; Reference number: A23982; MUID:86137403; PMID:3841523
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R;Fenton, S.P.; Lamande, S.R.; Hannagan, M.; Stacey, A.; Jaenisch, R.; Bateman, J.F.
Biochim. Biophys. Acta 1216, 469-474; 1993
A;Title: Genomic sequence of mouse COLIA1 encoding the collagen propeptides.
A;Reference number: S39789; MUID:94092741; PMID:8268229
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                                                                                         GEPGPTGLPGPPGERGGPGSRGFPGADGVAGPKGPAGERGSPGPA
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             Gaps
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        12;
        Indels
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    2;
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A;Molecule type: DNA
    Mismatches
    2
    Conservative
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Aintrons: 770/3; 788/3; 806/3; 842/3; 860/3; 878/3; 932/3; 968/3; 1004/3; 1022/3; 1058/? (Superfamily: collagen alpha 1(I) chain, fibrillar collagen carboxyl-terminal homology; CySuperfamily: collade coil; extracellular matrix; glycoprotein; heterotrimer; triple helix F;1-22/Domain: signal sequence #status predicted <SIG> F;23-151/Domain: amino-terminal propeptide #status predicted <PRO> F;30-89/Domain: von Willebrand factor type. C repeat homology <PRO> F;152-1453/Product: collagen alpha 1(I) chain #status predicted <AMG> F;1224-1453/Domain: fibrillar collagen carboxyl-terminal homology <PCC>
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C;Species: Gallus gallus (chicken)
C;Date: 12-Aug-1981 #sequence_revision 06-Jul-1982 #text_change 31-Mar-2000
C;Date: 12-Aug-1981 #sequence_revision 06-Jul-1982 #text_change 31-Mar-2000
C;Date: 12-Aug-1981 #sequence_revision 06-Jul-1982 #text_change 31-Mar-2000
R;Accession: Ag0458; Ag0857
Dixit, S.N.; Yu, W.; Seyer, J.M.; Kang, A.H.; Gross, J. Biochemistry 21, 2048-2055, 1982
Biochemistry 21, 2048-2055, 1982
A;Title: Amino acid sequence of chick skin collagen alphal(I)-CB8 and the complete priman A;Reference number: A90458; MUID:82231995; PMID:7093229
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A; Residues: 1.1036 <HIG>
A; Residues: 1.1036 <HIG>
A; Experimental source: SI
A; Note: this is the latest in a series of papers from these workers elucidating the sequence: Experimental source: M.J.
B; Eyre, D.R.; Glimcher, M.J.
B; Eyre, D.R.; Glimcher, M.J.
A; Title: Biother, Biothys. Res. Commun. 48, 720-726, 1972
A; Title: Evidence for a previously undetected sequence at the carboxyterminus of the alph A; Reference number: A90181; MUID:72243016; PMID:5047697
                                                                                                                                                                                                 an indirect
A; Molecule type: DNA
A; Residues: 1-80, E', 82-105, 'D', 107-185, 1031-1201, 'G', 1203-1218, 'E', 1220-1221, 'T',
B; Rhodes: K; Rippe, R.A; Umcara, A.; Nehls, M.; Brenner, D.A.; Breindl, M.
B; Rhodes: K; Rippe, R.A; Umcara, A.; Nehls, M.; Brenner, D.A.; Breindl, M.
Mol. Cell. Biol. 14, 5950-5960, 1994
A; Title: DNA methylation represses the murine alpha 1(1) collagen promoter by an in A; Reference number: 148300; MUID: 94344105; PMID: 8065328
A; Accession: 148300; MUID: 94344105; PMID: 8065328
A; Residues: preliminary; translated from GB/EMBL/DDBJ
A; Residues: DNA
A; Molecule type: DNA
A; Residues: 1-80, 'E', 82-105, 'D', 107-147 <REF>
A; Cross-references: EMBL: X54876; NID: 950486; PIDN: CAA38657.1; PID: 950487
C; Genetics:
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Pred. No. 4.5e-55;
1; Mismatches 5; Indels 12
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A; Molecule type: DNA
A; Residues: 630-640, A; 642-785 «VIKZ>
A; Residues: 630-640, A; 642-785 «VIKZ>
A; Cross-references: EMBL:X16158; NID:929951; PIDN:CAA34278.1; PID:91335024
PIDN:CAA34283.1; PID:91335023; PIDN:CAA34284.1; PID:91335024
R; Bogaert, R.; Tiller, G.E.; Weis, M.A.; Gruber, H.E.; Rimoin, D.L.; Cohn, D.H.; Eyre, D
A; Title: An amino acid substitution (Gly853--5Glu) in the collagen alpha 1(II) chain pro
A; Reference number: A44309; MUID:93054548; PMID:1429602
A; Accession: A44309
                                  A/rosserior.

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A;Residues: 188-189, Xx, 191-195;1224-1230, Xx, 1232-1236 <DIA>
R;Franc, S.; Marzin, E.; Boutillon, M.M.; Lafont, R.; Lechene de la Forte, P.; Herbage,
Bischem. 234, 125-131, 1995
A;Title: Immunohistochemical and biochemical analyses of 20000-25000-year-old fossil car
A;Reference number: S63514; MUID:96096730; PMID:8529631
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A; Residues: 171-172, °C', 174-175 <ALA>
A; Residues: 171-172, °C', 174-175 <ALA>
A; Residues: 171-172, °C', 174-175 <ALA>
B; Note: untants sequence from a family with family with primary generalized osteoarthriti
R; Diab, M; Wu, J.J.; Eyre, D.R.
Biochem. J 314, 327-332, 1996
A; Title: Qollagen type IX from human cartilage: a structural profile of intermolecular c
A; Reference number: $64673; MUID:96195147; PMID:8660302
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A; Residues: 243-261;575-590;756-763, X7,765-779 <FRA>
A; Residues: 243-261;575-590;756-763, X7,765-779 <FRA>
A; Residues: 243-261;575-590;756-763, X7,765-779 <FRA>
A; Tiler, G.E.; Weis, M.A.; Polumbo, P.A.; Gruber, H.E.; Rimoin, D.L.; Cohn, D.H.; Eyre, Am. J. Hum. Genet. 56, 388-395, 1995
A; Tille: An RNA-splicing mutation (G+SIVS20) in the type II collagen gene (COL2A1) in a A; Reference number: I38867; MUID:95150028; PMID:7847372
A; Reference number: I38867
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Residues: 440, G', 442-456, E', 458-480, 'P', 482-509 <TILL>
A; Cross-references: EMBL:U15195; NID:9557053; PIDN:AAB60370.1; PID:9557054
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A; Readudes: 104-157, P.,159-236 <SUM>
A; Readudes: 104-157, P.,159-236 <SUM>
A; Cross-references: GB:J03065; GB:M23660; GB:N25655; GB:M25730; GB:M32168;
A; Ala-Kokko, L.; Baldwin, C.T.; Moskowitz, R.W.; Prockop, D.J.
Proc. Natl. Acad. Sci. U.S.A. 87, 565-5689, 1990
A; Title: Single base mutation in the type II procollagen gene (COL2A1) as a cause of p
A; Reference number: A94227; MUID:90370826; PMID:1975693
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FEBS Lett. 250, 171-174, 1989
A.Title: Structural analyses of the polymorphic area in type II collagen gene.
A;Reference number: SOSOOO; MUID:89325561; PMID:2753125
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,Residues; 501-676,'A',678-763,'A',785-831,'PA',834,'F',836-1214 <RAM>
,Cross-references: EMBL:X13783; NID:g30037; PIDN:CAA32030.1; PID:g930050
A;Cross-references: EMBL:X16711; NID:g30040; PIDN:CAA34683.1; PID:g30041
A;Note: alternative gplice form 1
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Bubmitted to the EMBL Data Library, December 1988
A;Reference number: 804892
A;Accession: 804892
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CORRIGOR and the Annual Descrizor [validated] - human

O'Alternae names: procollagen alpha i(II) chain precursor splice form 1; collagen

O'Alternae names procollagen alpha i(II) chain precursor splice form 1; collagen

O'Alternae names controllagen alpha i(II) chain precursor splice form 1; collagen

O'Scrizor and the Alley of Alley 
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A;Residues: 7-28,'R',99-157,'P',159-440,'G',442-456,'B',458-640,'A',642-831,'PA',834,'F'
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                                                                Length 1042;
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                                                                Score 1067; DB 1;
Pred. No. 1.8e-52;
4; Mismatches 14;
                                                                90.1%;
llarity 86.4%;
Conservative
                                                                                                            Local Similarity
es 190; Conserv
                                                                Query Match
Best Local S:
Matches 190
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Accession and a general Section (A. 1917) 103, 57, 103-103, 17, 170-103, 103, 170-103, 103, 170-103, 170, 170-103, 170, 170-103, 170, 170-103, 170, 170-103, 170, 170-103, 170, 170-103, 170, 170-103, 170, 170-103, 170, 170-103, 170, 170-103, 170, 170-103, 170, 170-103, 170, 170-103, 170, 170-103, 170, 170-103, 170, 170-103, 170-103, 170-103, 170-103, 170-103, 170-103, 170-103, 170-103, 170-103, 170-103, 170-103, 170-103, 170-103, 170-103, 170-103, 170-103, 170-103, 170-103, 170-103, 170-103, 170-103, 170-103, 170-103, 170-103, 170-103, 170-103, 170-103, 170-103, 170-103, 170-103, 170-103, 170-103, 170-103, 170-103, 170-103, 170-103, 170-103, 170-103, 170-103, 170-103, 170-103, 170-103, 170-103, 170-103, 170-103, 170-103, 170-103, 170-103, 170-103, 170-103, 170-103, 170-103, 170-103, 170-103, 170-103, 170-103, 170-103, 170-103, 170-103, 170-103, 170-103, 170-103, 170-103, 170-103, 170-103, 170-103, 170-103, 170-103, 170-103, 170-103, 170-103, 170-103, 170-103, 170-103, 170-103, 170-103, 170-103, 170-103, 170-103, 170-103, 170-103, 170-103, 170-103, 170-103, 170-103, 170-103, 170-103, 170-103, 170-103, 170-103, 170-103, 170-103, 170-103, 170-103, 170-103, 170-103, 170-103, 170-103, 170-103, 170-103, 170-103, 170-103, 170-103, 170-103, 170-103, 170-103, 170-103, 170-103, 170-103, 170-103, 170-103, 170-103, 170-103, 170-103, 170-103, 170-103, 170-103, 170-103, 170-103, 170-103, 170-103, 170-103, 170-103, 170-103, 170-103, 170-103, 170-103, 170-103, 170-103, 170-103, 170-103, 170-103, 170-103, 170-103, 170-103, 170-103, 170-103, 170-103, 170-103, 170-103, 170-103, 170-103, 170-103, 170-103, 170-103, 170-103, 170-103, 170-103, 170-103, 170-103, 170-103, 170-103, 170-103, 170-103, 170-103, 170-103, 170-103, 170-103, 170-103, 170-103, 170-103, 170-103, 170-103, 170-103, 170-103, 170-103, 170-103, 170-103, 170-103, 170-103, 170-103, 170-103, 170-103, 170-103, 170-103, 170-103, 170-103, 170-103, 170-103, 170-103, 170-103, 170-103, 170-103, 170-103, 170-103, 170-103, 170-103, 170-103, 170-103, 170-103, 170-103, 170-103, 17
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Collagen alpha 1(II) chain precursor [imported] - horse

N.Alternate names: type II collagen

N.Alternate names: type II collagen

C.Species: Equal caballus (domestic horse)

C.Species: Squal caballus (domestic horse)

C.Accession: T45467

R.Richardson, D.W.; Dodge, G.R.

R.Richardson, D.W.; Dodge, G.R.

Submitted to the EMBL Data Library, June 1996

A.Description: Cloning of equine type II collagen and modulation of its expression in equal parts of the EMBL Data Library, June 1996

A.Reference number: 222977

A.Reference number: 222977

A.Reference type: MRNA

A.Molecule type: MRNA

A.Molecule type: MRIC>

A.Residues: 1-1418 - RIC>

A.Residues: 1-1418 - RIC>

A.Coss.references: EMBL: U62528; PIDN:AAB05773.1

C;Superfamily: collagen alpha 1(I) chain; fibrillar collagen carboxyl-terminal homology;
A;Cross-references: GB:M23759; NID:g180845; EMBL:X03320; GB:M24938; NID:g30104
A;Note: the GenBank PID is based on an incorrect reading frame
A;Accession: 137250
A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Molecule type: DNA
A;Cross-references: EMBL:X02378; GB:M23870; NID:g30107; PIDN:CAA26227.1; PID:g929621
A;Accession: 137251
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GEPGKAGERGVPGPPGAVGPAGKDGEAGAQGPPGPAGPAGERGEQGPAGSPGFQGLPGPA 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               482
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             552 GEPGLPGARGLTGRPGDAGPQGKVGPSGAPGEDGRPGPPGPQGARGQPGVMGFPGPKGAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       423 GARGEPGGAGPVGPPGERGAPGNRGFPGODGLAGPKGAPGERGPSGLAGPKGANGDPGRP
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llarity 74.0%; Pred. No. 6.4e-41;
Conservative 10; Mismatches 44; Indels
                                                                                                                                                                                                                                                                               Indels
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                                                                                                                                                                                                                                                                                  43;
                                                                                                                                                                                                                             72.8%; Score 862; DB 1;
74.0%; Pred. No. 5.1e-41;
ive 11; Mismatches 43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GPPGEAGKPGEQGVPGDLGAPGPSGPAG 208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                672 GPPGEGGKPGDÓGVPGEAGAPGLVGPRG 699
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                                                                                                                                                                                                                          Query Match
Best Local Similarity 74.0%
Matches 154; Conservative
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Matches 154; Conserv
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RESULT 9

A41182

collate: 28-May-1912 #sequence_revision 28-May-1992 #text_change 13-Aug-1999

C;Species: Mus musculus (house mouse)

C;Species: Mus musculus (house mouse)

C;Date: 28-May-1992 #sequence_revision 28-May-1992 #text_change 13-Aug-1999

R;Metsacanta, M.: 7coman, D.: 46 Crombrugghe, B.; Vuorio, E.

A;Reference number: A41182

A;Reference number: A41182

A;Residues: 1-1419 *MET>

A;Cross-references: GB:M65161

R;Cheah, K.S.; Lau, B.T.; Au, P.K.; Tam, P.P.

Development 111, 945-953, 1991

A;Title: Expression of the mouse alpha 1(II) collagen gene is not restricted to cartilage A;Accession, A44885; MUID:91347939; PMID:1879363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Cross-references: GB:M65161
C;Superfamily: collagen alpha 1(1) chain; fibrillar collagen carboxyl-terminal homology;
C;Reywords: alternative splicing; coiled coil; extracellular matrix; glycoprotein; trime:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Accession: A44885
A;Molecule type: DNA
A;Cross-references: GB:S63190; NID:9234369; PIDN:AAB19627.1; PID:9234369
A;Note: sequence extracted from NCBI backbone (NCBIN:63190; NCBIP:63192)
C;Superfamily: oollagen alpha I(I) chain; fibrillar collagen carboxyl-terminal homology;
C;Keywords: alternative splicing; coiled coil; extracellular matrix; glycoprotein; trime;
F;1191-1419/Domain: fibrillar collagen carboxyl-terminal homology <FCC>
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919
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collagen alpha 1(II) chain precursor (long splice form) - mouse
cylagen alpha 1(II) chain precursor (long splice form) - mouse
C;Species: Mus musculus (house mouse)
C;Species: 28-May-1992 #sequence_revision 28-May-1992 #text_change 16-Jul-1999
C;Accession: B41182
R;Metsaeranta, M.; Toman, D.; de Crombrugghe, B.; Vuorio, E.
A;Title: Mouse type II collagen gene. Complete nucleotide sequence, exon st.
A;Reference number: A41182; MUID:91358489; PMID:1885613
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   617 GEPGKAGEKGLGGAPGLRGLPGKDGETGAQGPNGPAGPAGERGEQGPPGPSGFQGLPGPP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              604 GPPGEGGKOGDOGIPGEAGAPGLVGPRG 631
                                                                                                                                                     704
                                                                                                                         GSPGEGGKPGDQGVPGEAGAAGLVGPRG
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                                                                            181 GPPGEAGKPGEQGVPGDLGAPGPSGPAG
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Best Local Similarity 72.15
Matches 150; Conservative
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A, Status: preliminary; not
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A; Residues: 1-1487 <MET>
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C;Species: Xenopus laevis (African clawed frog)
C;Species: Afold33
R;Su, M.W.; Suzuki, H.R.; Bieker, J.J.; Solursh, M.; Ramirez, F.
J. Call Biol. 115, S65-575, 1991
A;Title: Expression of two nonallelic type II procollagen genes during Xenopus laevis em A;Reference number: A40333
A;Status: nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 1-1492 <SUA>
A;Residues: 1-1492 <SUA>
A;Residues: 1-1492 cSUA>
A;Residues: 1-1492 cSUA>
C;Cores references: GBM:M63596
A;Note: this sequence is presented as substitutions relative to another sequence in a fise they replace; the appropriate interpretation of the sequence figure was reconstructed C;Superfamily: collagen alpha 1(I) folain; fibrillar collagen alpha 1(I) folain; fibrillar collagen atrix; glycoprotein; trimer; triple helix F;37-96/Domain: von Willebrand factor type C repeat homology <WC>
F;1263-1492/Domain: fibrillar collagen carboxyl-terminal homology <FCC>
                                                                                                                                                                 e
E
                                                                                                                                                                                                                                                                                                                                                                                                                                homology
                                        C,Accession: B40333
R,Su, M.W.; Suzuki, H.R.; Bieker, J.J.; Solursh, M.; Ramirez, F.
J. Cell Biol. 115, 565-575, 1991
A,Title: Expression of two nonallelic type II procollagen genes during Xenopus laevis A,Reference number: A40333; MUID:92011898; PMID:19181853
A,Accession: B40333
                                                                                                                                                                                                                                                                   A; Status: preliminary
A; Molecule type: mRNA
A; Molecule type: mare typ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GBAGLPGAKGLTGSPGSPGFDGKTGPPGPAGQDGRPGPPGPPGARGQAGVMGFPGPKGAA 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              120
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            10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              614 GEPGKAGEKGLVGAPGLRGLPGKDGETGSQGPNGPAGPAGEAGEQGPPGPSGFQGLPGPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 GPPGEPGPTGLPGPPGERGGPGSRGFPGADGVAGPKGPAGERGSPGPAGPKGSPGEAGRP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     494 GARGEPGAAGPNGPPGERGAPGNRGFPGQDGLAGPKGAPGERGVPGLGGPKGCNGDPGRP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GEAGLPGAKGLTGSPGSPGPDGKTGPPGPAGQDGRPGPPGPPGARGQAGVMGFPGPKGAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ouery Match
71.8%; Score 850; DB 1; Length 1486;
Best Local Similarity 73.1%; Pred. No. 2.4e-40;
Matches 152; Conservative 11; Mismatches 45; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          46; Indels
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Pred. No. 3.5e-40;
9; Mismatches 46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GPPGEAGKPGEQGVPGDLGAPGPSGPAG 208
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153; Conserv
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Best Local S:
Matches 153
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A; Molecule type: protein
A; Residues: 676-758 <F14>
A; Residues: 676-758 <F14>
A; Residues: 676-758 <F14>
A; Experimental source: skin
A; Note: Pro-726 is the only 3-hydroxyproline and the only hydroxylated proline in positic
B; Rauterberg, 0.; Fietzek, P.; Rexrodt, F.; Becker, U.; Stark, M.; Kuehn, K.
FEBS Lett. 21, 75-79, 1972
A; Title: The amino acid sequence of the carboxyterminal nonhelical cross link region of t
A; Reference number: A43048

A,Accession: A43048 A,Molecule type: protein A,Residues: 759-779 <RA2>

A;Title: The covalent structure of collagen. Amino acid sequence of peptide alphal-CB6-C; A;Reference number: A91200; MUID:73042275; PMID:4343807

A; Accession: A91200

Experimental source: Skin (274, 346, 424, 496, 658, and 670 may be hydroxy comment: Lysines at positions 115, 124, 274, 346, 424, 496, 658, and 670 may be hydroxy cycomment: Prolines in the third position of the tripeptide repeating unit (G-X-Y) are hy (CCOmment: Prolines in the third position of the alpha 1(1) chain of bovine skin or 9, 149, 268, and 217 residues.

Cycomment: The complete chain contains 1052 residues.

Cycomment: The complete chain contains 1052 residues.

Cycomment: The complete chain sontains 1(1) chain; fibrillar collagen carboxyl-terminal homology; Cykeywords: colled coll; extracellular matrix, glycoprotein; pyroglutamic acid; trimer; F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

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                                                                                                                                                                                                                                                                              121 GEPGKAGERGVPGPPGAVGPAGKDGEAGAQGPPGPAGPAGERGEQGPAGSPGFQGLPGPA 180
                                                                                                                                                                                                                                                                                                       9
                                                                                                                                1 GPPGEPGPTGLPGPPGERGGPGSRGFPGADGVAGPKGPAGERGSPGPAGPKGSPGEAGRP
                                                                                                                                                         492 GARGEPGGAGPIGPPGERGAPGNRGFPGODGLAGPKGAPGERGPSGLAGPKGANGDPGRP
                                                                                                                                                                                                                                            552 GEPGLPGARGLTGRPGDAGPQGKVGPSGAPGEDGRPGPPGPQGARGQPGVMGFPGPKGAN
                                                                                                Gaps
F;33-91/Domain: von Willebrand factor type C repeat homology <VWC>F;1259-1487/Domain: fibrillar collagen carboxyl-terminal homology <FCC>
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                                                                                              46;
                                                       70.9%; Score 839; DB 72.1%; Pred. No. 9.6e-ive 12; Mismatches
                                                                                                                                                                                                                                                                                                                                                           181 GPPGEAGKPGEQGVPGDLGAPGPSGPAG 208
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                                                                                              Conservative
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A,Residues: 1-19 <RAU>
A,Experimental source: skin
                                                                          Best Local Similarity
Matches 150; Conser
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                                                         Query Match
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A,Note: the epsilon carbon of Lys-9, by homology with the rat alpha 1(I) chain, is conversitetzek, P.P.; Kuehn, K.
B.Fietzek, P.P.; Kuehn, K.
Blochem. 52, 77-82, 1975
A;Itle: The covalent structure of collagen: amino-acid sequence of the cyanogen-bromide A;Reference number: A91229; MUID:76022320; PMID:1164916
A;Accession: A91229
collagen alpha 1(I) chain - bovine (tentative sequence) (fragments)
(Species: Bos primigenius taurus (cattle)
(C;Date: 24-Apr-1984 #sequence_revision 31-Dec-1993 #text_change 31-Mar-2000
C;Date: 24-Apr-1994 #sequence_revision 31-Dec-1993 #text_change 31-Mar-2000
C;Accession: A91193; A91293; A91319; A91211; A91201; A91200; A43048; A02853
R;Rauterberg, J.; Timpl, R.; Furthmayr, H.
Bur. J. Bloohem. 27, 231-237, 1972
A;Title: Structural characterization of N. terminal antigenic determinants in calf and lakeference number: A91193; MUID:72255334; PMID:4115172
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GLPGPAGPPGEAGKPGEQGVPGDLGAPGPSGPAG 208 GLPGPAGPPGEAGKPGEQGVPGDLGAPGPSGARG 242

175

89 GARGLPGTAGLPGMKGHRGFSGLDGAKGDAGPAGPKGEPGSPGENGAPGQMGPRGLPGFP

54 88

. 9

50;

Query Match
69.6%; Score 824; DB 1.
Best Local Similarity 72.0%; Pred. No. 4e-39;
Matches 154; Conservative 4; Mismatches 5

Length 779; Indels 1 GPPGEPGPTGLPGPPGERGGPGS-----RGFPGADGVAGPKGPAGERGSPGPAGPKGSP GPPGAPGPQGFQGPPGEPGEPGASGPMGPRGPPGPPGRNGDDGEAGKPGRPGERGPPGPQ 55 GEAGRPGEAGLPGAKGLTGSPGSPGPDGKTGPPGPAGODGRPGPPGPPGAKGQAGVMGFP

29

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A; Molecule type: protein
A; Residues: 1.15 cMLL>
A; Residues: 1.15 cMLL>
A; Residues: 1.15 cMLL>
A; Residues: 1.15 cMLL>
A; Note: residues positioned by comparison with human alpha 1(II) chain
B; Butler, W.T.; Miller, E.J.; Finch Jr., J.E.
Biochemistry 15, 3000-3006, 1976
A; Title: The covalent structure of cartilage collagen. Amino acid sequence of the NH-2-te
A; Reference number: A90396; MUID:7625364; PMID:782511
A; Contents: fragments CNBr2 (16-18), CNBr3 (19-21), CNBr6 (22-54), CNBr12 (55-138), and t Colligen alpha 1(II) chain precursor - bovine (tentative sequence) (fragments)
Cyspecies: Bos primigenius taurus (cattle)
Cybate: 24-Apr-1984 #sequence revision 17-May-1996 #text change 31-Mar-2000
CyAccession: A90369; A90396; A9210; S03940; A90189; A05039; A02859
CyAccession: LJ, Lunde, L. G.
Biochemistry 12, 3153-3159, 1973
A;Title: Isolation and characterization of the cyanogen bromide peptides from the alphalmatcher: composition of CNBrl and CNBr4
A;Contents: composition of CNBrl and CNBr4
A;Accession: A90369; A,Molecule type: protein A,Residues: 16-177 <BUT> A,Experimental source: cartilage A,Note: order of CNBr peptides determined R,Butler, W.T.; Finch Jr., J.E.; Miller, E. A, Accession: A90396 ਸ਼ The amino-acid sequence of the 112 residues A, Molecule type: protein
A, Residues: 146-294 <FIZ>
A, Experimental source: skin
A, Experimental source: skin
B, Fietzek, P.P.; Rexrodt, F.W.; Hopper, K.E.; Kuehn, K.
Eur. J. Biochem. 38, 396-400, 1973
A, Title: The covalent structure of collagen. 2. The amino-acid sequence of alphal-CB7
A, Reference number: A91211; MUID: 74086118; PMID: 4359390

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A.Molecule type: protein A.Residues: 563-675 <WEN> A.Experimental source: skin R.Fietzek, P.P.; Rexrodt, F.W.; Wendt, P.; Stark, M.; Kuehn,

A,Accession: A91211
A,Molecule type: protein
A,Residues: 295-562 <F13A;Residues: 295-562 <F13A;Experimental source: skin
R;Wendt, P.; Mark, K.V.D.; Rexrodt, F.; Kuehn, K.
Eur. J. Biochem. 30, 169-183, 1972
A;Title: The covalent structure of collagen. The amino-a
A;Reference number: A91201; WUID:73042276; PMID:4343808
A;Accession: A91201

517 111 577 171 637

51

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A;Molecule type: protein
A;Residues: 288-291,'P', 293-294,'X',296-297;606,'X',608-617 <MOR>
R;Weil, D.; Bernard, M.; Gargano, S.; Ramirez, F.
Mucleic Acids Res. 15, 181-198, 1987
A;Title: The pro alpha 2(V) collagen gene is evolutionarily related to the major fibrill?
A;Reference number: A25874; MUID:87146331; PMID:3029669
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                                                      A,Accession: 150694
A,Status: preliminary; translated from GB/EMBL/DDBJ
A,Status: preliminary; translated from GB/EMBL/DDBJ
A,Status: preliminary; translated from GB/EMBL/DDBJ
A,FORDAS-references: EMBL:U07973; NID:G520454; PIDN:AAA83407.1; PID:G537432
C;Genetics:
A;Genetics:
A;Gene
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R; Greenspan, D.S.; Lee, S.T.; Lee, B.S.; Hoffman, G.G.
Gane Expr. 1, 29-39, 1991
A; Title: Homology between alpha2(V) and alpha1(III) collagen promoters and evidence for A; Reference number: A54555; MUID:92314691; PMID:1820205
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R;Moradi-Ameli, M.; Rousseau, J.C.; Kleman, J.P.; Champliaud, M.F.; Boutillon, M.M.;
Bur. J. Biochem. 22, 987-955; 1995
Faur. J. Biochem. 22, 1987-955; 1995
Afritle: Diversity in the processing events at the N-terminus of type-V collagen.
A;Reference number: S43642; MUID:94237164; PMID:8181482
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          collagen alpha 2(V) chain precursor - human collagen Homo sapiens (man) C;Species: Homo sapiens (man) C;Species: Homo sapiens (man) C;Species: Homo sapiens (man) C;Species: Joul-1995 #sequence_revision 28-Jul-1995 #text_change 31-Dec-2000 C;Accession: A;1427; A54555; S4643; A25874; I55239; I59025; A25374; A30017 R;Woodbury, D.; Benson-Chanda, V.; Ramirez, F. J. Biol. Chem. 264, 2735-2738, 1989 A;Title: Amino-terminal propeptide of human pro-alpha2(V) collagen conforms A;Reference number: A31427.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          458 GPPGEEGKRGANGEPGONGVPGTPGERGSPGFRGLPGSNGLPGEKGPAGERGSPGPPGPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   52 GSPGEAGRPGEAGLPGAKGLTGSPGSPGPDGKTGPPGPAGQDGRPGPPGPPGARGQAGVM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   112 GFPGPKGAAGEPGKAGERGVPGPPGAVGPAGKDGEAGAQGPPGPAGPAGERGEQGPAGSP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 GPP------GEPGPTGLPGPPGERGGPGSRGFPGADGVAGPKGPAGERGSPGPAGPK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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A.Residues: 398-1496 <MEI>
A.Cross-references: GB:X04759; NID:g29588; PIDN:CAA28454.1; PID:g1340175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Molecule type: mRNA
A;Residues: 1-463 <WOO>
A;Cross-references: GB:J04478; NID:g179697; PIDN:AAA51859.1; PID:g179698
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         172 GFQGLPGPAGPPGEAGKPGEQGVPGDLGAPGPSGPAG 208
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      67.1%; Score 794.5; DB 2;
65.9%; Pred. No. 1.9e-37;
iive 13; Mismatches 52;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Experimental source: rhabdomyosarcoma cell line R; Myers, J.C.; Loidl, H.R.; Stolle, C.A.; Seyer, J.M. J. Biol. Chem. 260, 5533-5541, 1985
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity 65.9 143; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Molecule type: DNA; Residues: 1-32 <GRE>
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Best Local S
Matches 143
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J. Biol. Chem. 252, 639-641, 1977

A. Tille: Inte Covalent structure of cartilage collagen. Evidence for sequence heterogeneis A. Accession: A9210; MUDI:7703364; PMID:833147

A. Accession: A92210; MUDI:7703364; PMID:833147

A. Accession: A92210; MUDI:7703364; PMID:833147

A. Moseidule type: protein

A. Moseid
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Cispecies: Gallus gallus (chicken)
Cispecies: Gallus gallus (chicken)
Cispecies: 13-5ep-1996 #sequence_revision 13-5ep-1996 #text_change 13-Aug-1999
Ciscossion: 150694
Rinah, H.D.; Niu, Z.; Adams, S.L.
J. Biol. Chem. 269, 16443-16448, 1994
A;Title: An alternative transcript of the chick type III collagen gene that does
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      367 GEAGL PGAKGLTGR PGDAG PQGKVGPSGAPGEDGR PGPPGPQGARGQ PGVHGF PGPKGAN 426
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GEPGKAGERGVPGPPGAVGPAGKDGEAGAQGPPGPAGFRGERGEQGPAGSPGFQGLPGPA 180
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Best Local Similarity 78.9%; Pred. No. 1.1e-38;
Matches 146; Conservative 4; Mismatches 35; Indels
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collagen alpha 1(III) chain precursor - human
N;Alternate names: procollagen alpha 1(III) chain
C;Spates sapiens (man)
C;Date: 24-Apr-1984 #sequence revision 01-Sep-1995 #text change 21-Jul-2000
C;Accession: S05272; S04642; PE0011; S01726; S04887; A90399; A94562; I51868; S59511; A904
Submitted to the EMBL Data Library, February 1989
A;Reference number: S05272
A;Accession: S05272
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A, Modecule type: mRNA
A, Modecule type: mRNA
A, Residues: 1-1240, V, 1242-1466 <PRC>
A, Cross-references: EMBL:X14420; NID:G30057; PIDN:CAA32583.1; PID:G30058
B, Ala-Kokko, L., Kontusaarari, S., Baldwin, C.T.; Kuivaniemi, H.; Prockop, D.J.
Biochem. J. 260, 509-516, 1989
A, Title: Structure of cDNA clones coding for the entire prepro-alphal(III) chain of humar
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R;Toman, P.D.; Ricca, G.A.; de Crombrugghe, B.
Rvicleic Acids Res. 16, 7201, 198
A;Title: Nucleotide sequence of a cDNA coding for the amino-terminal region of human preg.
A;Reference number: S01726; MUID:88303360; PMID:3405773
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A;Molecule type: mRNA
A;Residues: 1-1196 Alb.
A;Residues: 1-1196 Alb.
A;Cross-references: EMBL:X14420; NID:g30057; PIDN:CAA32583.1; PID:g30058
A;Note: the complete sequence is not shown
R;Benson-Chanda, V.; Su, M.W.; Weil, D.; Chu, M.L.; Ramirez, F.
A;7, 255-265, 1989
A;Title: Cloning and analysis of the 5' portion of the human type-III procollagen gene
A;Reference number: PE0011; MUID:89378752; PMID:2777083
                  F;201/Modified site: allysine (lys) #status predicted
F;290,293,296,608,614,1004,1007,1013,1028,1034/Modified site: 4-hydroxyproline (Pro): F;299,1139/Modified site: 5-hydroxylysine (Lys) #status predicted
F;299,1139/Painding site: carbohydrate (Lys) (covalent) #status predicted
F;1029/Modified site: 5-hydroxylysine (Lys) #status experimental
F;1259,1139/Painding site: carbohydrate (Asn) (covalent) #status predicted
F;1259,1397/Painding site: carbohydrate (Asn) (covalent) #status predicted
F;1259,1397/Painding site: carbohydrate (Asn) (covalent) #status predicted
F;1293,1299,1325/Paisulfide bonds: interchain #status predicted
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A;Residues: 1-170 -470A
A;Crosa-references: EMBL:X07240; NID:g30060; PIDN:CAA30229.1; PID:g30061
A;Note: the authors translated the codon CAG for residue 154 as His
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ·.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 66.4%; Score 786; DB 1; Length 1496; Best Local Similarity 67.3%; Pred. No. 8.3e-37; Matches 140; Conservative 15; Mismatches 53; Indels (
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A;Residues: 1-176 <BEN>
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C/SUPPERTAINTY: collagen alpha I(I) chain; fibrilar collagen carboxyl-terminal homology;
C/SUPPERTAINTY: collagen alpha I(I) chain; fibrilar collagen carboxyl-terminal homology;
C/SUPPERTAINTY: collagen alpha I(I) chain; fibrilar collagen carboxyl-terminal homology;
C/STY-105/Domain: signal sequence #status predicted <SIG>
F/27-125/Product: collagen alpha 2(V) chain #status predicted <WAT>
F/27-125/Prediction: nonhelical
F/30-126/Region: nonhelical
F/30-126/Region: cell attachment (R-G-D) motif
F/30-125/Region: cell attachment (R-G-D) motif
F/30-1059/Region: cell attachment (R-G-D) motif
F/30-1050/Region: cell attach
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A Molecule type: mRNA
A Residues: 1003-1034 (RES-
A) Residues: 1003-1034 (RES-
A) Residues: 1003-1034 (RES-
A) Residues: 1003-1034 (RES-
A) Note: part of this sequence were determined by protein sequencing
A) Note: part of this sequence were determined by protein sequencing
A) Note: part of this sequence were determined by protein sequencing
A) Note: part of this sequence were determined by protein sequencing
A) Note: part of this sequence of the human alpha-2 type V procollagen COOH-termine
A) Reference number: A25374
A) Residue type: mRNA
A) Residues: 1227-1417, T, 1419-1437, S, 1439-1496 (ANYE)
A) Residues: 1227-1417, T, 1419-1437, S, 1439-1496 (ANYE)
A) Residues: 1227-1417, MID: 9180912; PIDN: AAAS2058.1; PID: 9180913
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A)Accession: A30017
A)Molecule type: DNA
A)Molecule the authors translated the codon GAA for residue 1460 as Gln, and GAG for residu Comment: Prolines and lysines at the third position of the tripeptide repeating unit (are 5-hydroxylated and subsequently O-glycosylated.
C)Comment: The amino-terminal propeptide domain appears not to be completely cleaved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A.Cross-references: GDB:119064; OMIM:120190
A;Map position: 2431-2431
A;Map position: 2431-2431
C;Entrope Signature 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      on the long arm
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               R;Tsipouras, P.; Schwartz, R.C.; Liddell, A.C.; Salkeld, C.S.; Weil, D.; Ramirez, F. Genomics 3, 275-27, 1988
A;Title: Genetic distance of two fibrillar collagen loci, COL3A1 and COL5A2, located A;Reference number: A30017; MUID:89138450; PMID:3224983
                               2 type V collagen chain.
A,Title: Partial covalent structure of the human alpha 2 type V collagen of A,Reference number: 155239; MUID:85182703; PMID:2985598
A,Reference number: 155239
A,Status: translated from GB/EMBL/DDBJ
A,Molecule type: mRNA
A,Molecule type: mRNA
A,Residues: 1002-1226 cRE2
A,Cross-references: GB.M10956; NID:g180427; PIDN:AAA52007.1; PID:g180428
A,Note: part of this sequence were determined by protein sequencing
R;Emanuel, B.S.; Cannizzaro, L.A.; Seyer. J. M.; Myers, J.C.
Proc. Natl. Acad. Sci. U.S.A. 82, 3385-3389, 1985
A,Title: Human alpha 1 (III) and alpha 2 (V) procollagen genes are located cA,Reference number: 159025; MUID:85216505; PMID:3858826
A,Status: translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Gene: GDB: COL5A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C,Genetics:
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A, Map position: 2431-2431
A, Introns: 27/1; 94/3; 11/3; 149/3; 176/3; 584/3; 587/3; 1175/3; 1275/1; 1337/3; 1418/3
A, Introns: 27/1; 94/3; 111/3; 140/3; 156/3; 587/3; 1175/3; 1275/1; 1337/3; 1418/3
A, Note: the list of introns is incomplete; defects in this gene can result in Ehlers-Danl C, Complex: type III collagen is a homotrimer of monomers initially linked by disulfide bc er of their length, is formed with desmosine cross-links made from lysine and allysine re
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Description: structural component of extracellular fibrous polymer that maintains integ C; Superfamily: collagen alpha 1(1) chain; fibrillar collagen carboxyl-terminal homology; C; Keywords: coiled coil; Ehlers-Danlos syndrome; extracellular matrix; glycoprotein; hydi
                                                                       A, Molecule type: mRNA
A, Residues: 861-1015 < COL>
A, Residues: 861-1015 < COL>
A, Cross-references: 861-105617; GB:MS5603; GB:MS9227; NID:g180878; PIDN:AABS9383.1; PID:g1
A, Note: a mutant sequence with 942-977 spliced out from a patient with Ehlers-Danlos sync
R; Mankco, B.S.; Dalqleish, R.
Nucleic Acids Res. 16, 2337, 1988
A; Title: Human pro alpha1(III) collagen: cDNA sequence for the 3' end.
A; Reference number: S02119; MUID:88189827; PMID:3357782
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Molecule type: protein A; Molecule type: protein A; Molecule type: protein A; Molecule type: protein A; Molecule type: 919,4,'PS',981-984,'PS',987,'QN',990-1096,'P',1098-1152,'AT',1155,'S',1157-3, A; Molecule A; Molecul
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Kesidues: 1161-1200 <MIS>
A;Cross-references: GB:M13146; NID:g180415; PIDN:AAA52003.1; PID:g180416
B;Emanuel, B.S.; Cannizzaro, L.A.; Seyer, J.M.; Myers, J.C.
B;Emanuel, B.S.; Cannizzaro, L.A.; Seyer, J.M.; Myers, J.C.
A;Title: Human alpha 1(III) and alpha 2(V) procoollagen genes are located on the long arm A;Reference number: IS9025; MUID:85216505; PMID:3858826
A;Accession: I79359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A,Note: the authors translated the codon TTC for residue 1057 as Tyr; the codons given for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; Comment: Prolines and lysines at the third position of the tripeptide repeating unit (^{(c)}3-hydroxylated. About 15% of the lysines are 5-hydroxylated and some are subsequently ^{(c)}
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Miskulin, M.; Dalgleish, R.; Kluve-Beckerman, B.; Rennard, S.I.; Tolstoshev, P.; Brant, inchemistry 25, 1408-1413, 1986
inchemistry 25, 1408-1413, 1986
inchemistry 25, 1408-1413, 1986
inchemistry 25, 1408-1413, 1986
inchemistry 25, 111 collagen gene expression is coordinately modulated with the type inchemical number: 152393; MUID: 86187804; PMID: 3754462
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A;Residues: 1176-1240, VV, 1242-1356, 'P', 1358-1466 <CHU>
A;Cross-references: GB:M10615; GB:M10793; GB:M10794; GB:M10795; GB:M10796; GB:M10797;
A;Experimental source: liver
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Status: translation not shown
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Cross-references: BmBL:X06700; NID:g30053; PIDN:CAA29886.1; PID:g30054
B;Seyer, J.M.; Kang, A.H.
B;Seyer, J.M.; Kang, A.H.
A;Seyer, J.M.; Kang, A.H.
A;Title: Covalent structure of collagen: amino acid sequence of alphal (III)-CB9:A;Reference number: A90446; MUID:81208139; PMID:7016180
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*Readdues: 1165-1196 *ENA>

*Cross-references: GB:M11134; NID:g180417; PIDN:AAA52004.1; PID:g180418

*Chu, M.L.; Weil, D.; de Wet, W.; Bernard, M.; Sippola, M.; Ramirez, F.

*E Biol. Chem. 260, 4357-4363, 1985

*Title: Isolation of CDNA and genomic clones encoding human pro-alphal(I

*Reference number: A92516; MUID:85157600; PMID:2579949
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A; Cross-references:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Accession: A92516
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Accession: A93551
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National Res (19
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F;1-23/Domain: signal sequence #status predicted <SIG>
F;2-153/Domain: anino-terminal propeptide #status predicted <PRO>
F;24-153/Domain: anino-terminal propeptide #status predicted <PRO>
F;154-1221/Product: collagen alpha 1(III) chain #status predicted <MAT>
F;154-1221/Product: collagen alpha 1(III) chain #status predicted <MAT>
F;154-1221/Product: collagen alpha 1(III) chain #status predicted <APA
F;163-196/Region: amino-terminal nonhelical telopeptide
F;163-1221/Region: carboxyl-terminal nonhelical telopeptide
F;1031-1033/Region: carboxyl-terminal nonhelical telopeptide
F;1223-1466/Domain: carboxyl-terminal propeptide #status predicted
F;1238-1466/Domain: fibrillar collagen carboxyl-terminal homology <PRC>
F;1238-1466/Domain: fibrillar collagen carboxyl-terminal homology <PRC>
F;1238-1466/Domain: fibrillar collagen N-endopeptidase) #status predicted
F;153-154/Cleavage site: pyrrolidone carboxylic acid (Gln) (in mature form) #status predicted
F;153,284/Rodified site: allysine (Lys) #status predicted
F;263,284/Rodified site: allysine (Lys) #status experimental
F;263,284/Rodified site: 5-hydroxylysine (Lys) (partial) #status experimental
F;948-949/Cleavage site: Gly-Ile (collagenase) #status experimental
F;948-949/Cleavage site: Gly-Ile (covalent) #status experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 65.5%; Score 776; DB 1; Length 1466; Best Local Similarity 66.3%; Pred. No. 2.9e-36; Matches 138; Conservative 12; Mismatches 58; Indels (
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468 61

Db ò dd ð Search completed: September 24, 2004, 11:11:45 Job time : 9.04914 secs

181 GPPGEAGKPGEQGVPGDLGAPGPSGPAG 208 GPPGENGKPGEPGPKGDAGAPGAPGKG 675

648

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1 GPPGEPGPTGLPGPPGERGGPGSRGFPGADGVAGPKGPAGERGSPGPAGPKGSPGEAGRP 60

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INPORMATION FOR SEQ ID NO: 18: SEQUENCE CHARACTERISTICS: LENGTH: 1341 amino acids TYPE: amino acids TYPE: amino acids TOPOLOGY: linear NOLECULE TYPE: protein ORIGINAL SOURCE: ORGANISM: Homo sapiens IMMEDIATE SOURCE: CLONE: CLO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            18, Appl

9, Appl

19, Appl

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11, Appl

12, Appl

12, Appl

13, Appl

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16, Appl

17, Appl

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Seguence 18, Appl
                                                                                                                                                                                             September 24, 2004, 11:06:56; Search time 8.60425 Seconds (without alignments) 1254.011 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                              US-10-658-989A-1
1184
1 GPPGEPGPTGLPGPPGERGG......GEQGVPGDLGAPGPSGPAGG 209
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1: /cgn2_6/prodate3/laa/5A_COMB.pep:*
/cgn2_6/prodate3/laa/5B_COMB.pep:*
3: /cgn2_6/prodata3/laa/6A_COMB.pep:*
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5: /cgn2_6/prodata3/laa/PCTUS_COMB.pep:*
6: /cgn2_6/prodata3/laa/PCTUS_COMB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-09-500-811-18
US-09-550-811-18
US-09-5548-608-18
US-09-585-887-9
US-09-219-849-48
US-09-219-849-48
US-09-219-849-48
US-09-219-849-49
US-09-500-811-20
US-09-548-608-20
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US-08-468-996-11
US-08-963-825-21
US-09-570-871-21
US-09-570-573-21
US-09-548-608-21
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         389414 seqs, 51625971 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                    OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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seq length: 200000000
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Match Length DB
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Perfect score: 1
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sequence 10, Appl Sequence 2, Appli Sequence 19, Appl Sequence 19, Appl Sequence 19, Appl Sequence 19, Appl Sequence 65, Appl Sequence 65, Appl Sequence 65, Appl Sequence 52, Appl Sequence 52, Appl Sequence 51, Appl Sequence 52, Appl Sequence 53, Appl Sequence 54, Appli Sequence 53, Appli Sequence 53, Appli Sequence 53, Appli Sequence 64, Appli Sequence 65, Appli Sequence 65, Appli Sequence 66, Appli Sequence 67, Appli Sequence 67, Appli Sequence 61, Appli Sequence 61, Appli		lagen Fragments t and Means for Carrying Out thod to Diagnose the Presence of the Metabolism of the Metabolism of 1.25
66 4 US-09-585-887-10 66 4 US-09-585-887-10 66 3 US-08-963-825-2 66 4 US-08-963-825-19 66 4 US-09-548-60-19 66 4 US-09-548-60-19 66 4 US-09-548-60-19 67 1 US-08-42-255-32 08 3 US-08-475-411A-65 08 3 US-08-475-411A-65 09 3 US-08-475-411A-65 01 US-08-65-255-51 01 US-08-642-255-51 02 US-08-642-255-51 03 US-08-642-255-51 04 US-08-642-255-51 05 US-08-642-255-51 07 US-08-642-255-51 08 US-08-642-255-51 08 US-08-642-255-51 08 US-08-642-255-51 08 US-08-642-255-51 08 US-08-642-255-51 08 US-08-642-255-51 08 US-08-642-255-51 08 US-08-642-255-51	ALIGNMENTS	n US/08963825 er latrin A Method for Assaying Collagen in Body Fluids, A Test Kit and Method and Use of the Method to Disorders Associated with the M 21 iss: & Darby PC Avenue PC-DOS/MS-DOS IR Release #1.0, Version #1.25 DATA: IN Release #1.0, Version #1.25 DATA: IN SO8/963,825 IN SO8/187,319 RAN-1994 WATION: RR: 29,714 UWABER: 4305/08701 FURBER: 4305/08701 FORMATION: RR: 29,7700 6237
745 62.9 136 744 62.9 136 744 62.8 136 744 62.8 136 744 62.8 136 657 55.5 136 657 55.5 4 655.5 55.4 5 656.5 55.4 5 648 54.7 77 648 65.5 65.6 65.6 65.6 65.6 65.6 65.6 65.		RESULT 1 Sequence 18, Application US/0896382 Sequence 18, Application US/0896382 Patent No. 6110689 GENERAL INFORMATION: APPLICANT: Bonde, Martin APPLICANT: Bonde, Martin TITLE OF INVENTION: A Method for TITLE OF INVENTION: in Body FlutTILE OF INVENTION: Method and TITLE OF INVENTION: A Method and TITLE OF INVENTION: Disorders A NUMBER OF SEQUENCES: 21 CORRESPONDENCE ADDRESS: ADDRESSEE: Darby & Darby PC STREET: New York COUNTRY: New York COUNTRY: USA ZIP: 10022 COMPUTER: NEW APPL COMPUTER: Darby disk COMPUTER: Darby disk COMPUTER: Darby disk COMPUTER: Darby Weber STREET: New York COMPUTER: DARBESS: ADDIO TYPE: COMPUTER: 15M PC COMPATION COMPUTER: DARBESS: APPLICATION NUMBER: US/08/963 FILING DATE: CLASSIFICATION NUMBER: US/08/187 FILING DATE: 21-JAN-1994 ATTORNEY/AGENT INFORMATION: NAME: AGGOTIS, Adda RECISTRATION NUMBER: 29,714 RECISTRATION NUMBER: 29,714 RELEPAN: 212-577-7700 TELLEFAN: 212-577-7700
8 0 0 H G W 4 B B B B B B B B B B B B B B B B B B	-16	RESULT 18-608-96 (Section 18-608-96) (Section

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Fri Sep 24 11:45:38 2004

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A Method for Assaying Collagen Fragments in Body Fluids, A Test Kit and Means for Carrying Out the Method and Use of the Method to Diagnose the Presence of Disorders Associated with the Metabolism of
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                                                                                                                          Gaps
                                                                                                                          12;
                 Length 1341;
                                                                                                                          Indels
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     97.0%; Score 1149; DB 4; 33.6%; Pred. No. 2e-72; iive 0; Mismatches 2;
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PRIOR APPLICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/187,319
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: 29.714
REPERENCE/DOCKET NUMBER: 4305/087
TELECOMMUNICATION INFORMATION:
TELEPRANCE CLASSIFICATION:
TELEPRANCE CLASSIFICATION:
TELEPRANCE CLASSIFICATION:
TELEPRANCE CLASSIFICATION:
TELER PAX: 23.6687
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CLASSACTION:
LENGTH: 1141 amino acids
TYPE: amino acids
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APPLICATION NUMBER: US/09/570,573
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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Patent No. 6342361
GENERAL INFORMATION:
APPLICANT: QVISt, Per
APPLICANT: Bonde, Martin
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805 Third Avenue
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CLONE: COLLAGEN ALPHA 1 (I)
Query Match
Best Local Similarity 93.6'
Matches 206; Conservative
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DB 4; Length 1341;

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393 48

us-10-658-989a-1.rai

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| PARENT NO. 6413/42|
| GENERAL INFORMATION |
| APPLICANT: Chang, Robert |
| APPLICANT: Chang, Robert |
| APPLICANT: Chang, Robert |
| APPLICANT: Chisholm, George |
| TITLE OF INVENTION: NOVEL METHODS FOR THE PRODUCTION OF GELATIN AND |
| TITLE OF INVENTION: CPLL. LENGTH TRIPLE HELICAL COLLAGEN IN RECOMBINANT; TITLE OF INVENTION: CPLL. LENGTH TRIPLE HELICAL COLLAGEN IN RECOMBINANT; TITLE OF INVENTION: CPLL. SOUGH |
| FILE REFERENCE: 25002030400 |
| CURRENT APPLICATION NUMBER: 09/289,578 |
| PRICR FILING DATE: 1999-06-09 |
| PRICR FILING DATE: 1999-06-08 |
| NUMBER OF SEQ ID NOS: 11 |
| SEQ ID NO 9 |
| LENGTH: 1461
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Gaps
12;
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Indels
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Pred. No. 2.2e-72;
  0; Mismatches
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Best Local Similarity 93.6%;
Matches 206; Conservative
    206; Conservative
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ORGANISM: Homo sapiens
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US-09-585-887-9
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                                                                                                                                                                                                                                                                                       GPKGSPGEAGRPGEAGLPGAKGLTGSPGSPGPDGKTGPPGPAGQDGRPGPPGARGQA 108
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                                                                      -GEPGPTGLPGPPGERGGPGSRGFPGADGVAGPKGPAGERGSPGPA
                             Gaps
                             12;
                          Indels
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/548,608
FILING DATE:
                          2;
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Pred. No. 2e-72;
Pred. No. 2e-72;
                          0; Mismatches
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/187,319
FILING DATE:
ATTORNEY AGENT INFORMATION:
NAME: GOGOLIS, Adda C
REGISTRATION NUMBER: 29,714
REFERENCE/DOCKET NUMBER: 4305/08
TELEPHONE: 212-527-700
TELEFAX: 212-527-700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 18, Application US/09548608
Patent No. 6355442
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: Darby & Darby PC STREET: 805 Third Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: amino acid
TOPOLOGY: 1.**
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INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 1341 amino acids
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  93.6%;
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CLONE: COLLAGEN ALPHA 1
                          Matches 206; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: protein ORIGINAL SOURCE:
                                                                        1 GPP-----
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STATE: New York
COUNTRY: USA
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Best Local Similarity
    Best Local Similarity
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US-09-548-608-18
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                                                                                                                                    578 GVMGFPGPKGAAGEPGKAGERGVPGPPGAVGPAGKDGEAGAQGPPGPAGPAGERGEQGPA 637
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: Assay for collagen degradation NUMBER OF SEQUENCES: 4
COMPUTER READABLE FORM: A COMPUTER READABLE FORM: MEDIUM TYPE: PLOPDY disk .
COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO) CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/931,820 FILING DATE: CLASSIFICATION: 435 PRICK APPLICATION: 435 PRICK APPLICATION: ASPECATION TO BATA: APPLICATION DATA: APPLICA
                                                                                                                                                                                                                              169 GSPGFQGLPGPAGPPGEAGKPGEQGVPGDLGAPGPSGPAG 208
                                                                                                                                                                                                                                                                                  638 GSPGFQGLPGPAGPPGEAGKPGEQGVPGDLGAPGPSGARG 677
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Patent No. 6150081
GENERAL INFORMATION:
APPLICANT: VAN HEERDE, GEORGE V.
APPLICANT: VAN RIJN, ALEXIS C.
APPLICANT: BOUWSTRA, JAN B.
                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 8
US-08-931-820-1
; Sequence 1, Application US/08931820
; Patent No. 6010863
; GENERAL INFORMATION:
; APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          mo sapiens
Collagen type I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INFORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS: LENGTH: 1057 amino acid: TYPE: amino acid: STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: protein
HYPOTHETICAL: NO
ANTI-SENSE: NO
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US-09-219-849-48
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Sequence 21, Application US/09331347C
Sequence 21, Application US/09331347C
Sequence 21, Application US/09331347C
Sequence 21, Application US/09331347C
GENERAL INFORMATION:
APPLICANT: Meristem Therapeutics, S.A.
APPLICANT: Meristem Therapeutics, S.A.
TITLE OF INVENTION: Recombinant Collagens and Derived Proteins Produced by Plants, N TITLE OF INVENTION: Obtaining Such and Their Uses
TILE REPERBUCE: 1149-3
CURRENT APPLICATION NUMBER: US/09/331,347C
CURRENT FILING DATE: 1999-08-17
NUMBER OF SEQ ID NOS: 22
SOFTWARE: PatentIn version 3.1
APPLICANT: Olsen, David R
APPLICANT: Chang, Robert
APPLICANT: Chang, Robert
APPLICANT: Chang, Robert
APPLICANT: McMullin, Hugh
APPLICANT: Hitzeman, Romald A.
APPLICANT: Chisholm, George
TITLE OF INVENTION: NOVEL METHODS FOR THE PRODUCTION OF GELATIN AND
TITLE OF INVENTION: FULL.LENGTH TRIPLE HELICAL COLLAGEN IN RECOMBINANT
TITLE OF INVENTION: CELLS
FILE REFERENCE: 225002030400
CURRENT PAPLICATION NUMBER: US/09/289,578
CURRENT PILING DATE: 1999-04-10
PRIOR APPLICATION NUMBER: 60/084,828
PRIOR PLLING DATE: 1998-05-08
NUMBER OF SEQ ID NOS: 11
SCPTWARE: Patentin Ver. 2.0
SEQ ID NOS: 11
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97.0%; Score 1149; DB 4; Length 1461;
Best Local Similarity 93.6%; Pred. No. 2.2e-72;
Matches 206; Conservative 0; Mismatches 2; Indels 12
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97.0%; Score 1149; DB 4; Length 1464;
Best Local Similarity 93.6%; Pred. No. 2.2e-72;
Matches 206; Conservative 0; Mismatches 2; Indels 12
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ORGANISM: Homo sapiens
US-09-331-347C-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Homo sapiens
US-09-289-578-9
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LENGTH: 1464
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Query Match
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Matches 199,
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APPLICANT: DE WOLF, FREDERIK A.
APPLICANT: MOCORGEK, ANDREAS
APPLICANT: WERTEN, MARC W.C.
APPLICANT: WIND, RICHELE D.
APPLICANT: WIND, RICHELE D.
TITLE OF INVENTION: SILVER HALIDE EMULSIONS WITH RECOMBINANT COLLAGEN
TITLE OF INVENTION: SUITABLE FOR PHOTOGRAPHIC APPLICATION AND ALSO THE
TITLE OF INVENTION: PREPARATION THEREOF
FILE REPRENCE: 2728-2
CURRENT APPLICATION NUMBER: US/09/219,849
CURRENT APPLICATION NUMBER: US/09/219,849
CURRENT FILING DATE: 1998-12-23
NUMBER OF SEQ ID NOS: 50
SEQ ID NO 48
LENGTH: 595
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CRGANISM: Artificial Sequence
FEATURE:
COTHER INFORMATION: Description of Artificial Sequence: Synthetic
COTHER INFORMATION: amino acid sequence
US-09-219-849-50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FRATURE:
COTHER INFORMATION: Description of Artificial Sequence: Synthetic
COTHER INFORMATION: amino acid sequence
CS-09-219-849-48
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94.3%; Score 1116; DB 3; Length 595;
Best Local Similarity 90.5%; Pred. No. 1.9e-70;
Matches 199; Conservative 4; Mismatches 5; Indels 1
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Sequence 50, Application US/09219849

Patent No. 6150081

GENERAL INFORMATION

APPLICANT: VAN HEEDE, GEORGE V.

APPLICANT: BOUWSTRA, JAN B.

APPLICANT: BOUNSTRA, JAN B.

APPLICANT: BOUNSTRA, JAN B.

APPLICANT: WERNERA, MARCA W.T.

APPLICANT: WENDER, ANDREAS

APPLICANT: WIND, RICHELE D.

APPLICANT: WIND, SUITABLE FOR PHOTOGRAPHIC A.

ITILE OF INVENTION: SUITABLE FOR PHOTOGRAPHIC A.

ITILE OF INVENTION DATE: 1998-12-23

NUMBER OF SEQ ID NOS: 50

IENGHH S. 595
                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT
ORGANISM: Artificial Sequence
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US-09-219-849-50
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APPLICANT: VAN HEERDE, GEORGE V.
APPLICANT: VAN HEERDE, ALEXIS C.
APPLICANT: VAN RIJN, ALEXIS C.
APPLICANT: BOUNGTRA, JAN B.
APPLICANT: BOUNGTRA, JAN B.
APPLICANT: BOUNGTRA, MADREAS
APPLICANT: WERTEN, MARC W.T.
APPLICANT: WIND, RICHELE D.
APPLICANT: WIND, RICHELE D.
APPLICANT: WIND, RICHELE D.
APPLICANT: WIND, RICHELE D.
APPLICANT: WIND ROSCH, TANJA J.
APPLICANT: WIND ROSCH, TANJA J.
APPLICANT: WIND ROSCH, TANJA J.
APPLICANT: WAND WIND STRUE FOR PHOTOGRAPHIC APPLICATION AND ALSO THE TITLE OF INVENTION: PREPARATION THEREOF
FILE REPERENCE: 2728-2
CURRENT APPLICATION NUMBER: US/09/219,849
CURRENT APPLICATION WORDER: 198-12-23
NUMBER OF SEQ ID NOS: 50
SOFTWARE: PALCHLIN VEY: 2.1
SEQ ID NO 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ä
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                                                                                                                                                                                338
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                                                                                                                                                                                                                                         49 GPKGSPGEAGRPGEAGLPGAKGLTGSPGSPGPDGKTGPPGPAGQDGRPGPPGARGQA 108
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                                                                                                                                                                                                                                                                                                                                                                                                      399 GVMGFPGPKGTAGEPGKAGERGLPGPPGAVGPAGKDGEAGAGAGGAPGPAGPAGFRGEQGPA 458
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                                                                                                                                                                                                                                                                                279 GPPGPAGEEGKRGARGEPGPSGLPGPPGERGGPGSRGFPGADGVAGPKGPSGERGAPGPA
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                                                                                                                      1 GPP------GEPGPTGLPGPPGERGGPGSRGFPGADGVAGPKGPAGERGSPGPA
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                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OTHER INFORMATION: Description of Artificial Sequence: Synthetic OTHER INFORMATION: amino acid sequence
                                                            12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 822;
   Length 595;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                            5; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       169 GSPGFQGLPGPAGPPGEAGKPGEQGVPGDLGAPGPSGPAG 208
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94.3%; Score 1116; DB 3;
Best Local Similarity 90.5%; Pred. No. 2.6e-70;
Matches 199; Conservative 4; Mismatches 5;
Score 1116; DB 3;
Pred. No. 1.9e-70;
4; Mismatches 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-09-219-849-49; Application US/09219849; Sequence 49, Application US/09219849; Patent No. 6150081.
FEBREAL INFORMATION:
APPLICANT: VAN HEERDE, GEORGE V.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Artificial Sequence
Match
Local Similarity 90.5%;
tes 199; Conservative 4
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61 GEAGLPGAKGLTGSPGSPGFDGKTGPPGPAGQDGRPGPPGPPGARGQAGVMGFPGPKGAA 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                121 GEPGKAGERGVPGPPGAVGPAGKDGEAGAQGPPGPAGPAGERGEQGPAGSPGFQGLPGPA 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 73.1%; Score 866; DB 4; Length 1017; Best Local Similarity 74.5%; Pred. No. 6.6e-53; Matches 155; Conservative 11; Mismatches 42; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO) CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/931,820
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: Assay for collagen degradation NUMBER OF SEQUENCES: 4
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  472 GPPGEAGKPGDQGVPGEAGAPGLVGPRG 499
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                                                CURRENT FILING DATE: 2003-02-07

PRIOR APPLICATION NUMBER: US 07/843,752

PRIOR FILING DATE: 1992-02-28

PRIOR FILING DATE: 1990-02-21

PRIOR FILING DATE: 1990-02-21

PRIOR FILING DATE: 1990-02-21

PRIOR PILING DATE: 1990-10-15

PRIOR PILING DATE: 1990-10-15

PRIOR PILING DATE: 1990-10-15

PRIOR PILING DATE: 1990-02-20

PRIOR PILING DATE: 1980-05-20

PRIOR PILING DATE: 1980-03-02

PRIOR PILING DATE: 1980-03-02

PRIOR APPLICATION NUMBER: US 07/487,732

PRIOR APPLICATION NUMBER: US 07/851,632

PRIOR APPLICATION NUMBER: US 07/551,632

PRIOR FILING DATE: 1990-03-02

PRIOR FILING DATE: 1990-03-02

PRIOR FILING DATE: 1990-03-02

PRIOR FILING DATE: 1990-03-02

PRIOR FILING DATE: 1990-10-31

PRIOR PILING DATE: 1900-10-31

PRIOR PILING DATE: 1900-10-31
FILE REFERENCE: 1010/16959-US3
CURRENT APPLICATION NUMBER: US/08/468,996
CURRENT FILING DATE: 2003-02-07
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CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 96202596.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-08-931-820-3
; Sequence 3, Application US/08931820
; Patent No. 6010863
; GENERAL INFORMATION:
; APPLICANT:
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; ORGANISM: Homo sapiens US-08-468-996-10
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                                                Patent No. 6645504
GENERAL INFORMATION:
APPLICANT: Willer, Ariel
APPLICANT: Miller, Ariel
APPLICANT: Annad, Al-Sabbagh
TITLE OF INVENTION: BYSTANDER SUPPRESSION OF TYPE 1 DIABETES BY ORAL ADMINISTRATION OF TITLE OF INVENTION: GLUCACON
FILE REPERENCE: 1010/16599-90153
CURRENT APPLICATION NUMBER: US/08/468,996
CURRENT FILING DATE: 2003-02-07
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APPLICANT: Miller, Ariel
APPLICANT: Zheng, Zhengi
APPLICANT: Zheng, Zhengi
APPLICANT: Ahmad, Al-Sabbagh
TITLE OF INVENTION: BYSTANDER SUPPRESSION OF TYPE 1 DIABETES BY ORAL ADMINISTRATION -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GPKGSPGEAGRPGEAGLPGAKGLTGSPGSPGPDGKTGPPGPAGQDGRPGPPGPPGAKGQA 108
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                                                                                                                                                                                                                                                                                                                                                              PRIOR FILING DATE: 2020-202-8
PRIOR FILING DATE: 1992-02-28
PRIOR FILING DATE: 1992-02-28
PRIOR FILING DATE: 1990-02-21
PRIOR APPLICATION NUMBER: US 07/460,852
PRIOR APPLICATION NUMBER: US 07/596,936
PRIOR FILING DATE: 1990-10-15
PRIOR FILING DATE: 1990-10-15
PRIOR FILING DATE: 1997-6-24
PRIOR FILING DATE: 1997-6-24
PRIOR FILING DATE: 1990-10-15
PRIOR PRILICATION NUMBER: US 07/487,732
PRIOR FILING DATE: 1990-03-02
PRIOR FILING DATE: 1990-07-10
PRIOR FILING DATE: 1990-07-10
PRIOR FILING DATE: 1990-07-14
PRIOR FILING DATE: 1990-07-14
PRIOR FILING DATE: 1990-07-14
PRIOR FILING DATE: 1990-10-31
PRIOR FILING DATE: 1990-10-10
NUMBER OF SEQ 1D NOS: 13
SEQ 1D NO 12
                        Sequence 12, Application US/08468996 Patent No. 6645504
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Patent No. 6645504
GENERAL INFORMATION:
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Best Local Similarity 76.0°
Matches 165, Conservative
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ORGANISM: Bos taurus
JS-08-468-996-12
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Search completed: September 24, 2004, 11:09:49 Job time : 10.6042 secs
                                                                                                                                     ; INMEDIATE SOURCE:
; CLONE: COLLAGEN -ALPHA 1 (II)
US-08-963-825-20
                         1418 amino acids
                                                                                                                                                                                                                                           Query Match
Best Local Similarity 74.0%
Matches 154; Conservative
                                                                                                                                  Homo sapiens
                                            TYPE: amino acid
TOPCLOGY: linear
MOLECULE TYPE: protein
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
SEQUENCE CHARACTERISTICS
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TITLE OF INVENTION: in Body Fluids, A Test Kit and Means for Carrying Out the
TITLE OF INVENTION: Method and use of the Method to Diagnose the Presence of
TITLE OF INVENTION: Disorders Associated with the Metabolism of
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSE: Darby & Darby PC
                                                                                                                                                                                                                                                                                                                                                                                 311 GARGEPGGVGPIGPPGERGAPGNRGFPGQDGLAGPKGAPGERGPSGLAGPKGANGDPGRP 370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       431 GEPGKAGEKGLPGAPGLRGLPGKDGETGAEGPPGPAGPAGERGEGGAPGPSGPGGPGPP 490
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    121 GEPGKAGERGVPGPPGAVGPAGKDGEAGAQGPPGPAGPAGERGEQGPAGSPGFQGLPGPA 180
                                                                                                                                                                                                                                                                                                                                                         1 GPPGEPGPTGLPGPPGERGGPGSRGFPGADGVAGPKGPAGERGSPGPAGPKGSPGEAGRP
                                                                                                                                                                                                                                                                Ouery Match 72.8%; Score 862; DB 3; Length 1060; Best Local Similarity 74.0%; Pred. No. 1.3e-52; Matches 154; Conservative 11; Mismatches 43; Indels
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CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10022
COMPUTER: READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US/08/963,825
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            181 GPPGEAGKPGEQGVPGDLGAPGPSGPAG 208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION: 436
PRIOR APPLICATION DATA.
APPLICATION NUMBER: US/08/187,319
FILING DATE: 21-JAN-1994
ATTCNREY/AGENT INFORMATION:
NAME: GGGOTIS, Adda C
REGISTRATION NUMBER: 29,714
REPERRENCE/DOCKET NUMBER: 4305/08701
TELEPHONE: 212-527-7700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 20, Application US/08963825
Patent No. 6110689
GENERAL INFORMATION:
APPLICANT: Qvist, Per
APPLICANT: Bonde, Martin
                                                                                                                                                                                   mo sapiens
Collagen type II
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              E: Darby & Darby PC
805 Third Avenue
                         LENGTH: 1060 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                        TOPOLOGY: linear

MOLECULE TYPE: protein

HYPOTHETICAL: NO

ORIGINAL SOURCE:

GRGANISM: Homo sapiens

TISSUE TYPE: Collagen type: 0931-220-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: 212-753-6237
TELEX: 236687
INFORMATION FOR SEQ ID NO:
    SEQUENCE CHARACTERISTICS:
LENGTH: 1060 amino aci
TYPE: amino acid
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US-08-963-825-20
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                                                                                                                                                                                                                                                                                                                                         543 GEPGKAGEKGLPGAPGLRGLPGKDGETGAEGPPGPAGPAGERGEGGAPGPSGFQGLPGPP 602
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                                                Gaps
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  Length 1418;
                                                   43; Indels
72.8%; Score 862; DB 3; 74.0%; Pred. No. 1.7e-52; ive 11; Mismatches 43
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ALIGNMENTS
                                        ADD14142
ADD45059
ADD45051
ADE87048
AAE02535
AAE02532
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                                                                                                                                                                                           AAB68057 standard; protein; 501 AA
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09-JUL-2001
AAB68057;
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2065.614 Million cell updates/sec
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1 GPPGEPGPTGLPGPPGERGG......GEQGVPGDLGAPGPSGPAGG 209
      GenCore version 5.1.6 (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                        Total number of hits satisfying chosen parameters:
                                                                                                                            1586107 seqs, 282547505 residues
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Maximum Match 100%
Listing first 45 summaries
                                 - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Sequence:

protein

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Run on:

Scoring table:

Searched:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

geneseqp2004s:

Collagen/ Amino aci Collagen/ A chimeri Human pan Recombina Amino aci A human c Amino aci Collagen/ Amino aci Human pan Collagen Collagen Human col Collagen Amino aci Collagen/ Human pre Aab68057 Amino aci Aae02703 Human alp Description Aay84544 Aay84403 Aar894403 Aar894540 2 Aar89459 0 Aar89469 Aar894537 Aar894537 Aar894537 Aar89470 Aar89470 Aar89470 Aay84538 Ade87057 Aar894707 Aays6800 H Abg93947 H Aaw68485 H Aab82454 H Adb84290 I Aay84541 / Abb80733 (Abb09625) SUMMARIES AABC02703 ADB44290 AAB44290 AAX44544 AAX84403 AAX84403 AAX89469 AAX89469 AAX89463 AAX89463 AAX89470 AAX89470 AAX89470 AAX701701 AAX701701 AAX701701 AAX701701 AAX701701 AAX701701 AAX809733 ABR80733 AAX809733 AAX809733 AAY56800 ABG93947 AAW68485 AAB82454 AAB68057 DB Length Query Match Result

26 1149 97.0 1464 4 AAU14136 28 1149 97.0 1464 5 ABB90764 29 1149 97.0 1464 6 ABB90764 30 1149 97.0 1464 6 ABR4471 31 1149 97.0 1464 7 ADD14142 32 1149 97.0 1464 7 ADD14142 33 1149 97.0 1464 7 ADD14142 34 1149 97.0 1464 7 ADD45055 35 1149 97.0 1464 7 ADD45055 36 1149 97.0 1464 7 ADD45051 37 1149 97.0 1464 7 ADB87048 38 1144 96.6 1449 4 AAB02535 40 1122 94.8 1453 7 ADD45053 41 1122 94.8 1453 7 ADD45054 42 1122 94.8 1453 7 ADD45054 44 1122 94.8 1453 7 ADD45054 45 1122 94.8 1453 7 ADD45054
1149 97.0 1464 1149 96.6 1449 1122 94.8 1453 1122 94.8 1453
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for The present sequence represents a human recombinant gelatin polypeptide. The recombinant gelatin polypeptide is used to produce vaccine formulations of the invention. The recombinant human gelatin is non-immunogenic (therefore reducing anaphylactic reactions) and confers stability at ambient temperatures. The vaccine formulation comprises a vaccine formulated for the prevention of a disease selected from vaccinia virus (small pox), polio virus (salk and Sabin), mumps, measles, rubella, Vaccine formulations (I) comprising recombinant human gelatin, useful for vaccinating against e.g. mumps, measles, rubella, tetanus, rabies and cholera, the gelatin is non-immunogenic and confers stability at ambient /note= "this residue is given as unknown as illegible in the specification" Polarek JW; Amino acid sequence of a recombinant human gelatin. Human; gelatin; vaccine; anaphylactic reaction. Olsen DR, Claim 11; Page 114-116; 130pp; English. Location/Qualifiers Neff TB, 12-NOV-1999; 99US-0165114P. 10-NOV-2000; 2000WO-US030843 Chang RC, Kivirikko KI, (FIBR-) FIBROGEN INC. WPI; 2001-308784/32. Misc-difference WO200134801-A2 temperatures. Homo sapiens 17-MAY-2001.

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diphtheria, tetanus, Varicella-Zoster (chicken pox/shingles), pertussis (whooping cough), Bacille Calmette-Geurin (BGG, tuberculosis), memorphilus influenzae meningitis, rabies, cholera, Japanese encephalitis virus, salmonella typhi, shigella, hepatitis A and B, adenovirus, yellow fever, foot and mouth disease, herpes simplex virus, respiratory syncytial virus, rotavirus, Dengue, West Nile virus, turkey herpes virus (Marek's disease), influenza and/or anthrax
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                                                                                                                                                                                                                        12;
                                                                                                                                                                                    97.0%; Score 1149; DB 4; Length 501;
illarity 93.6%; Pred. No. 3.5e-67; Conservative 0; Mismatches 2; Indels 1;
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15-MAY-2000; 2000US-0204437P.
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Best Local Similarity
Matches 206; Conserv
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The patent discloses recombinant human gelatin which is useful in various compositions including binding agents, encapsulants, stabilising agents, film-forming agents, moisturising agents, enclands film agents, colloidal agents, adhesive agents, pharmaceutical compositions, hard gel capsules, soft gel capsules, pharmaceutical compositions, harmaceutical stabilisers, micro-carriers, edible compositions, protein supplements, fat substitutes, nutritional compositions, protein supplements, fat substitutes, nutritional compositions, industrial composition, cell culture compositions and compositions for use in the laboratory. Pharmaceutical compositions and compositions such as architis, athrosis and other compising recombinant gelatin are used as vaccines. They are also used to treat various joint conditions such as arthritis, athrosis and other conditions related to the degeneration of cartilage and joint fluctures. The present sequence is human alphal (1) type I collagen industries. The present sequence is human alphal (1) type I collagen belical domain (residues 179-679). This sequence is a recombinant gelatin
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    hepatotropic; vaccine; recombinant gelatin; vaccinia virus; small pox; polio virus; Salk and Sabin; mumps; measles; rubella; diphtheria; retannus; Varicella-Zoster; chicken pox; shingles; pertussis; whopping cough; Bacille Calmette-Guerin; BGG; tuberculosis; Haemophilus influenzae; meningitis; rabies; cholera; cholera; Japanese encephalitis virus; Salmonella typhi; Shigella; hepatitis A; hepatitis B; adenovirus; yellow fever; foot and mouth disease; herpes simplex virus; respiratory syncytial virus; rotavirus; dengue; west Nile virus; Turkey herpes virus; Marek's disease; influenza;
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Matches 206; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 501 AA;
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12-NOV-1999;

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The specification describes a method for producing an extracellular matrix protein or its fragment. The extracellular matrix protein is capable of self aggregating in a cell which does not ordinarily hydroxylated prolines. The method comprises optimising a nucleic acid sequence for expression in the cell by substitution of codons preferred by the cell; of that cell for naturally occurring codons not preferred by the cell; incorporating the mucleic acid sequence into the cell; and contacting the cell with a hypertonic growth medium containing at least one amino acid; selected from the group consisting of trans-4-hydroxyproline and 3-hydroxyproline to allow at least one of the amino acids to be assimilated into the cell and incorporated into the extracellular matrix protein. The method may be used to make host cells assimilate and incorporate trans-4-hydroxyproline into proteins. This is especially useful in the recombinant production of proteins such as collagen, fibrinogen and fibronectin whose ability to self aggregate and produce functional proteins depends on the post translational hydroxyplation of proteins emethod is also useful in studying the structure and function of proteins because the structure and structure and structure and structure and structure the structure and structure and structure and structure and s
  trans-4-hydroxyproline, 3-hydroxyproline, recombinant protein production; collagen; fibrinogen; fibronectin; post translational hydroxylation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Production of extracellular matrix proteins containing 4-trans-hydroxyproline results in native self aggregating proteins, useful on medical implants.
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Matches 206; Conservative (
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N-PSDB; AAA12502.
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                                                                       Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        The invention describes a vaccine composition comprising a recombinant gelatin, and an antigenic agent. The vaccine can be delivered by infection, through masal, oral, transdermal or mucosal routes, or through dependences. Intravention of the composition intestinal, or parenteral (e.g. intraventicular, intraventicular, subcutaneous, intranedullary, intraocentescial, intraventicular, intraventicular, intraperitones, intranedullary, intraocentericular, intravences, intraperitones, intranedullary, intraocentar injection). The vaccine composition is formulated for the prevention of vaccinia virue (small pox), polio virue (salk and Sabin), mumps, meaales, rubella, diphtheria, tetanus, Varicella-Zoster (chicken pox/shingles), pertussis (whopping cough), Bacille Calmette-Guerin (BCG, tuberculosis), Haemophilus influenze meniggitis, rabies, cholera, dapances encephalitis virus, influence meningitis, rabies, cholera, dapances encephalitis virus, salmonella typhi, Shigella hepatitis A, hepatitis B, adenovirus, yellow fever, foot and mouth disease, hepres simplex virus, respiratory syncytial virus, rotavirus, dengue, Mest Nile virus, Turkey herpes virus (Marek's disease), influenza, and anthrax. This is the amino acid sequence of a recombinant gelatin used in the creation of a vaccine composition of the invention.
                                                                                                                                                                                                                                                                                                    New vaccine composition comprising a recombinant gelatin and an antigenic agent, useful for preventing e.g. polio virus, mumps, measles, rubella, diphtheria, tetanus, chicken pox/shingles, pertussis, cholera, rotavirus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 97.0%; Score 1149; DB 7; Length 501; Best Local Similarity 93.6%; Pred. No. 3.5e-67; Matches 206; Conservative 0; Mismatches 2; Indels 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Amino acid sequence of a human collagen 1 (alphal) protein.
                                                                                                                                                                                                             Polarek JW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          460 GSPGFQGLPGPAGPPGEAGKPGEQGVPGDLGAPGPSGARG 499
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             169 GSPGFQGLPGPAGPPGBAGKPGEQGVPGDLGAPGPSGPAG 208
                                                                                                                                                                                                             Olsen DR,
                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 16; Page 36-38; 63pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAY84541 standard; protein; 1057 AA.
                                                                                                                                                                                                           Neff TB,
  15-MAY-2000; 2000US-0204437P.
10-NOV-2000; 2000US-00710249.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                        Kivirikko KI,
                                                                CHANG R C.
KIVIRIKKO K I.
NEFF T B.
OLSEN D R.
                                                                                                                                                                                                                                                       WPI; 2003-540775/51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 501 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       25-JUL-2000
                                                                                                                                                                                                           Chang RC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        49
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAY84541;
                                                                                      (KIVI/)
(NEFF/)
(OLSE/)
                                                                                                                                                              (POLA/)
                                                                     (CHAN/)
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                                                                                                                                                                                                                            48
present sequence represents a human collagen 1 (alphal) protein, which may be produced using the method of the invention
                                                                                                                                                                                                                                                            49 GPKGSPGEAGRPGEAGLPGAKGLTGSPGSPGPDGKTGPPGPPGPAGODGRPGPPGPPGARGQA
                                                                                                                                                                                                                                                                                                                                                             357 GPKGSPGEAGRPGEAGLPGAKGLTGSPGSPGPDGKTGPPGPAGQDGRPGPPGPPGARGQA
                                                                                                                                                                                                                                                                                                                                                                                                                         109 GVMGFPGPKGAAGEPGKAGERGVPGPPGAVGPAGKDGEAGAQGPPGPAGPAGERGEQGPA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        417 GVMGFFGFKGAAGEPGKAGERGVPGPPGAVGPAGKDGEAGAQGPPGPAGERGEQGPA
                                                                                                                                                                                                                         1 GPP------GEPGPTGLPGPPGERGGPGSRGFPGADGVAGPKGPAGERGSPGPA
                                                                                                                                                                             Gaps
                                                                                                                                                                          12;
                                                                                                                        Length 1057;
                                                                                                                                                                          2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             169 GSPGFQGLPGPAGPPGEAGKPGEQGVPGDLGAPGPSGPAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       477 GSPGFOGLPGPAGPPGBAGKPGBOGVPGDLGAPGPSGARG
                                                                                                                        Score 1149; DB 3;
Pred. No. 6.4e-67;
0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 5
AAY84544
ID AAY84544 standard; protein; 1057
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(first entry)

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The specification describes a method for producing an extracellular matrix protein or its fragment. The extracellular matrix protein is capable of self aggregating in a cell which does not ordinarily hydroxylated prolines. The method comprises optimising a nucleic acid sequence for expression in the cell by substitution of codons preferred by that cell for naturally occurring codons not preferred by the cell; incorporating the nucleic acid sequence into the cell; and contacting the nucleic acid sequence into the cell; and contacting the cell with a hypertonic growth medium containing at least one amino acid, selected from the group consisting of trans-4-hydroxyproline and 3-hydroxyproline to allow at least one of the amino acids to be assimilated into the cell and incorporated into the extracellular matrix protein. The method may be used to make host cells assimilate and incorporate trans-4-hydroxyproline into proteins the sespecially useful in the recombinant production of proteins such as collagen, fibrinogen and proteins depends on the post translational hydroxylation of proline. The method is also useful in studying the structure and function of proteins depends which do not normally contain trans-4-hydroxyproline. The present sequence represents human collagen 1 (alphal) helical region, which may be produced using the method of the invention
                                                                                                                                              Extracellular matrix protein; self aggregation; hydroxylated proline; trans-4-hydroxyproline; 3-hydroxyproline; recombinant protein production; collagen; fibrinogen; fibronectin; post translational hydroxylation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Production of extracellular matrix proteins containing 4-trans-hydroxyproline results in native self aggregating proteins, useful on medical implants.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 97.0%; Score 1149; DB 3; Length 1057; Best Local Similarity 93.6%; Pred. No. 6.4e-67; Matches 206; Conservative 0; Mismatches 2; Indels 12.
                                                                                                       A human collagen 1 (alphal) protein helical region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Example 10; Fig 39A-E; 260pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        (USSU ) US SURGICAL CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI: 2000-259138/23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 1057 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    N-PSDB; AAA12503
                                                              25-JUL-2000
                                                                                                                                                                                                                                                                                                                                                                                                                 09-OCT-1998;
                                                                                                                                                                                                                                           sapiens
                                                                                                                                                                                                                                                                                                                                                                  07-OCT-1999;
                                                                                                                                                                                                                                                                                  EP992586-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gruskin BA,
                                                                                                                                                                                                                                                                                                                       12-APR-2000
                    AAY84544;
                                                                                                                                                                                                                                           Homo
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Connolly

Zhang G,

Buechter DD,

98US-00169768. 99EP-00119184.

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The present sequence represents a human type 1 (alphal) collagen protein. Peptides derived from the protien were used to demonstrate incorporation of 3.4-derydron-brolline into the peptide, using the method of the invention. The specification describes a method for the incorporation non-natural amino acid into a polypeptide. The method comprises reacting at least one 3.4-derydroprolline residue in the polypeptide with an epoxyprolline residue. The method is used for studying the effects of non-natural amino acids on structure and function of polypeptides. The method is also useful for commercial production of collagen or mussel adhesive proteins (which are useful as bloadhesives), and for incorporating a wice variety of groups, including therapeutic ligands and biological probes,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      109 GVMGFPGPKGAAGEPGKAGERGVPGPPGAVGPAGKDGEAGAQGPPGPAGPAGERGEQGPA 168
                                                                                                                                                                                                                                    Alphal collagen; 3,4-dehydro-L-proline; epoxidation; 3,4-epoxyproline; collagen; mussel adhesive protein; bioadhesive.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      298 GPPGPAGEEGKRGARGEPGPTGLPGPPGERGGPGSRGFPGADGVAGPKGPAGERGSPGPA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 358 GPKGSPGEAGRPGEAGLPGAKGLTGSPGSPGPDGKTGPPGPAGQDGRPGPPGPPGARGQA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 GPP-----GEPGPTGLPGPPGERGGPGSRGFPGADGVAGPKGPAGERGSPGPA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         49 GPKGSPGEAGRPGEAGLPGAKGLTGSPGSPGPDGKTGPPGPAGQDGRPGPPGARGQA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            e.9
                                                                                                                                                                                                      Amino acid sequence of human type 1 (alphal) collagen polypeptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Incorporating non-natural amino acid into polypeptide, useful production of bioadhesives, by epoxidation or substitution of dehydroproline residues.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 1058;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                477 GSPGFQGLPGPAGPPGEAGKPGEQGVPGDLGAPGPSGARG 516
169 GSPGFQGLPGPAGPPGEAGKPGEQGVPGDLGAPGPSGPAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 1149; DB 3;
Pred. No. 6.4e-67;
0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Buechter DD
                                                                                                          Ŕ
                                                                                                          AAY84403 standard; protein; 1058
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       English.
                                                                                                                                                                                                                                                                                                                                                                                 99WO-US020462.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             97.0%;
93.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                98US-0099652P
                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Paolella DN, Gruskin EA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure; Fig 6; 66pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                              US SURGICAL CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                             PACLELLA D N.
GRUSKIN E A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BUECHTER D D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2000-271051/23.
N-PSDB; AAZ99843.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  into polypeptides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 1058 AA;
                                                                                                                                                                                                                                                                                                                    WO200014201-A1
                                                                                                                                                                                                                                                                                                                                                                                                                09-SEP-1998;
                                                                                                                                                                                                                                                                                      Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                 07-SEP-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Simi
                                                                                                                                                                         12-JUL-2000
                                                                                                                                                                                                                                                                                                                                                   16-MAR-2000.
                                                                                                                                           AAY84403;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                ussu)
                                                                                                                                                                                                                                                                                                                                                                                                                                                               (PAOL/)
(GRUS/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BUEC/)
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                                                                                           AAY84403
                                                                              RESULT
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Gaps

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GPKGSPGEAGRPGEAGLPGAKGLTGSPGSPGPDGKTGPPGPAGQDGRPGPPGPPGARGQA 108

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GPKGSPGEAGRPGEAGLPGAKGLTGSPGSPGPDGKTGPPGPAGODGRPGPPGPPGARGQA

GVMGFPGPKGAAGEPGKAGERGVPGPPGAVGPAGKDGEAGAQGPPGPAGPAGERGEQGPA

109 417

à

GVWGFPGPKGAAGEPGKAGERGVPGPPGAVGPAGKDGEAGAQGPPGPAGPAGERGEQGPA

297 GPPGPAGEEGKKGARGEPGPTGLPGPPGERGGPGSRGFPGADGVAGPKGPAGERGSPGPA 356

---GEPGPTGLPGPPGERGGPGSRGFPGADGVAGPKGPAGERGSPGPA

GPP-----

48

108 357

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Gaps

12;

Indels

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Mismatches

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206; Conservative
    Matches
                                                                                                                                                                                                                                                 RESULT 8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Chimaeric DNA encoding protein contg. extracellular matrix protein domain - and cellular regulatory factor domain, partic. useful as osteogenic agents, also related vectors, transformed cells and chimaeric proteins.
A fusion protein (AAR89472) comprises the alpha-helical region of human collagen I(a) linked to amino acids 46-93 of human mature dermatan sulphate proteoglycan (decorin). It can be expressed in Escherichia colitransformants carrying a vector incorporating a chimeric gene (AAT16518) coding for the fusion. The decorin binds to type I collagen and thus affects Elbril formation. It inhibits the cell attachment-promoting activity of collagen and fibrinogen by binding to such molecules near their cell binding sites. The collagen moiety provides an integral substratum or scaffolding for the decorin. The fusion protein acts to reduce scarring of healing tissue
                                                                                                                                                                                                                                   Transforming growth factor; TGF-beta-1; collagen IA; osteogenesis; bone formation; tissue repair; fusion protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note= "amino acids P46 to G93 of mature decorin"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 1107;
                                                                                                                                                                                                                                                                                   Location/Qualifiers
1. .1057
/label= Collagen-IA
/note= "collagen IA alpha-helical domain"
887
                                       GSPGFOGLPGPAGPPGEAGKPGEQGVPGDLGAPGPSGPAG
                                                             GSPGFQGLPGPAGPPGEAGKPGEQGVPGDLGAPGPSGARG
                                                                                                                                                                                                                                                                                                                                                                 note= "unidentified amino acid"
                                                                                                                                                                                                                                                                                                                                                                                           acid"
                                                                                                                                                                                                                                                                                                                                                                                        note= "unidentified amino
                                                                                                                                                                                                         Collagen/decorin(aa46-93) fusion protein.
                                                                                                                                                                                                                                                                                                                                                                                                    1058. .1059
/label= Linker_peptide
1060. .1107
/label= Decorin
                                                                                                                               AAR89472 standard; protein; 1107 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Disclosure, Fig 8; 59pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    95CA-02151547.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              94US-00259263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            97.0%;
                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (USSU ) US SURGICAL CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Espino P;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 1996-140144/15.
                                                                                                                                                                                                                                                                                                                                                                               890
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    N-PSDB, AAT16518.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Seguence 1107 AA
                                                                                                                                                                                                                                                                                                                                                    Misc-difference
                                                                                                                                                                                                                                                                                                                                                                            Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    12-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           10-JUN-1994;
                                                                                                                                                                                  01-OCT-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gruskin EA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CA2151547-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          11-DEC-1995
                                                                                                                                                                                                                                                                         Synthetic
                                       169
                                                              478
                                                                                                                                                        AAR89472;
                                                                                                                                                                                                                                                                                                Key
Domain
                                                                                                                                                                                                                                                                                                                                                                                                      Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                Domain
                                                                                                                    AAR89472
                                                                                                      RESULT
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Score 1149; DB 2; Pred. No. 6.6e-67;

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matrix protein or its fragment. The extracellular matrix protein is capable of self aggregating in a cell which does not ordinarily dydroxylated prolines. The method comprises optimising a nucleic acid sequence for expression in the cell by substitution of codons preferred by that cell for naturally occurring codons not preferred by that cell for naturally occurring codons not preferred by the cell; incorporating the nucleic acid sequence into the cell; and contacting the cell with a hypertonic growth medium containing at least one amino acid, selected from the group consisting of trans-4-hydroxyproline and 3-hydroxyproline to allow at least one of the amino acids to be assimilated
                                                                                                                                                                                     476
                                                                         108
                                                                                                              416
                                                                                                                                                109 GVMGFPGPKGAAGEPGKAGERGVPGPPGAVGPAGKDGEAGAQGPPGPAGPAGFAGERGEQGPA 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Extracellular matrix protein; self aggregation; hydroxylated proline; trans-4-hydroxyproline; 3-hydroxyproline; recombinant protein production; collagen; fibrinogen; fibronectin; post translational hydroxylation; decorin; ohimera.
                                   297 GPPGPAGEEGKRGARGEPGPTGLPGPPGERGGPGSRGFPGADGVAGPKGPAGERGSPGPA 356
 48
                                                                                                357 GPKGSPGEAGRPGEAGLPGAKGLTGSPGSPGPDGKTGPPGPAGQDGRPGPPGPPGARGQA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Amino acid sequence of a chimeric collagen 1 (alphal)/decorin protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Production of extracellular matrix proteins containing 4-trans-
hydroxyproline results in native self aggregating proteins, useful on
medical implants.
                                                                         49 GPKGSPGEAGRPGEAGLPGAKGLTGSPGSPGPDGKTGPPGPAGQDGRPGPPGPPGARGQA
                                                                                                                                                                                   417 GVMGFPGPKGAAGEPGKAGERGVPGPPGAVGPAGKDGEAGAQGPPGPAGPAGERGEQGPA
1 GPP------GEPGPTGLPGPPGERGGPGSRGFPGADGVAGPKGPAGERGSPGPA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The specification describes a method for producing an extracellular
                                                                                                                                                                                                                                              477 GSPGFQGLPGPAGPPGEAGKPGEQGVPGDLGAPGPSGARG 516
                                                                                                                                                                                                                         GSPGFQGLPGPAGPPGEAGKPGEQGVPGDLGAPGPSGPAG 208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       몫
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note= "Gly encoded by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ω̈
                                                                                                                                                                                                                                                                                                                                                     AAY84540 standard; protein; 1107 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Zhang
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 24; Fig 18; 260pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           99EP-00119184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              98US-00169768
                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Key
Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens.
Unidentified.
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                                                                                                                                                                                                                         169
                                                                                                                                                                                                                                                                                                                                                                                          AAY84540;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Chimeric.
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                                                                                                                                                                                                                                                                                                                                                                                                                  method may be used to make host cells assimilate and incorporate trans-4-
hydroxyproline into proteins. This is especially useful in the
ecombinant production of proteins such as colladen, fibrinogen and
fibronectin whose ability to self aggregate and produce functional
proteins depends on the post translational hydroxylation of proline. The
method is also useful in studying the structure and function of
polypeptides which do not normally contain trans-4-hydroxyproline. The
present sequence represents a chimeric collagen 1 (alphal)/decorin
protein, which may be produced using the method of the invention
                                                                                                                                                                                                                               356
                                                                                                                                                                                                                                                                             357 GPKGSPGEAGRPGEAGLPGAKGLTGSPGSPGPDGKTGPPGPAGQDGRPGPPGARGQA 416
                                                                                                                                                                                                                                                                                                      GVMGFPGPKGAAGEPGKAGERGVPGPPGAVGPAGKDGEAGAQGPPGPAGPAGERGEQGPA 168
                                                                                                                                                                                                                                                                                                                       GWMGFPGPKGAAGEPGKAGERGVPGPPGAVGPAGKDGEAGAQGPPGPAGPAGERGEQGPA 476
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New pancreatic specific nucleic acid molecule or protein for diagnosing, staging, imaging, monitoring, preventing or treating pancreatic cancer or non-cancerous disease states of the pancreas.
                                                                                                                                                                                                                                                       GPKGSPGEAGRPGEAGLPGAKGLTGSPGSPGPDGKTGPPGPAGQDGRPGPPGPPGARGQA 108
and incorporated into the extracellular matrix protein. The
                                                                                                                                                                                                        8
                                                                                                                                                                                                        --GEPGPTGLPGPPGERGGPGSRGFPGADGVAGPKGPAGERGSPGPA
                                                                                                                                                                                                                                297 GPPGPAGEEGKRGARGEPGPTGLPGPPGERGGPGSRGFPGADGVAGPKGPAGERGSPGPA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This invention relates to novel nucleic acids and proteins present in normal and neoplastic pancreatic cells. Pancreatic cancer is a common
                                                                                                                                                                                12; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    neoplastic pancreatic cell, pancreatic cell, pancreatic cancer, cancer death, cytostatic, vaccine, gene therapy; non-cancerous pancreas disease, human.
                                                                                                                                                       Score 1149; DB 3; Length 1107; Pred. No. 6.6e-67; 0; Mismatches 2; Indels 12
                                                                                                                                                                                                                                                                                                                                                      GSPGFQGLPGPAGPPGEAGKPGEQGVPGDLGAPGPSGPAG 208
                                                                                                                                                                                                                                                                                                                                                                         GSPGFQGLFGPAGPPGEAGKPGEQGVPGDLGAPGPSGARG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human pancreatic cell protein sequence SeqID510.
                                                                                                                                                                                                                                                                                                                                                                                                                                        ADE87050 standard; protein; 1161 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 12; SEQ ID NO 510; 635pp;
                                                                                                                                                         97.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            19-DEC-2002; 2002WO-US040655.
                                                                                                                                                       Query Match
Best Local Similarity 93.6'
Matches 206; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                         1 GPP-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2003-587286/55.
N-PSDB; ADE87387.
                                                                                                                                  Sequence 1107 AA;
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                               and treatment are required. Compounds which modulate the proteins of the invention may have cytostatic activity and the protein and DNA sequences of the invention may be useful for the development of a vaccine or in gene therapy. The composition and methods are useful in diagnosing, staging, imaging, monitoring, preventing or treating pancreatic cancer and non-cancerous disease states of the pancreas. The present sequence is that of a human pancreatic protein of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            48
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           155 GPPGPAGEEGKRGARGEPGPTGLPGPPGERGGPGSRGFPGADGVAGPKGPAGERGSPGPA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               49 GPKGSPGEAGRPGEAGLPGAKGLTGSPGSPGPDGKTGPPGPAGQDGRPGPPGARGQA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   215 GPKGSPGEAGRPGEAGLPGAKGLTGSPGSPGPDGKTGPPGPAGQDGRPGPPGPPGARGQA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GVMGFPGPKGAAGEPGKAGERGVPGPPGAVGPAGKDGEAGAQGPPGPAGPAGERGEQGPA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       osteogenesis;
cause of cancer death worldwide, therefore accurate methods of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 1161;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
11. .1057
/label= Collagen-IA
/noce= "collagen IA alpha-helical domain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GSPGFQGLPGPAGPPGEAGKPGEQGVPGDLGAPGPSGPAG 208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    335 GSPGFQGLPGPAGPPGEAGKPGEQGVPGDLGAPGPSGARG 374
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 morphogenic protein 2B; BMP-2B; collagen IA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    97.0%; Score 1149; DB 7;
93.6%; Pred. No. 6.9e-67;
iive 0; Mismatches 2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                amino acid"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           unidentified and unidentified and unidentified and unide uni
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAR89469 standard; protein; 1169 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    95CA-02151547
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Matches 206; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 1161 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          11-DEC-1995
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAR89469;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Peptide
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Domain
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Connolly K;

ญั

Zhang

Buechter DD,

Gruskin EA,

WPI; 2000-259138/23

N-PSDB; AAA12497

(USSU) US SURGICAL CORP

98US-00169768

09-OCT-1998;

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Chimaeric DNA encoding protein contg. extracellular matrix protein domain - and cellular regulatory factor domain, partic. useful as osteogenic agents, also related vectors, transformed cells and chimaeric proteins.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           357 GPKGSPGEAGRPGEAGLPGAKGLIGSPGSPGPDGKIGPPGPAGQDGRPGPPGARGQA 416
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Extracellular matrix protein; self aggregation; hydroxylated proline; trans-4-hydroxyproline; 3.hydroxyproline; recombinant protein production; collagen; fibrinogen; fibronectin; post translational hydroxylation; ss. bone morphogenic protein; BMP-2B; chimera.
                                                                                                                                                                                                                                                                                                                                                                                                                              297 GPPGPAGEEGKRGARGEPGPTGLPGPPGERGGPGSRGFPGADGVAGPKGPAGERGSPGPA 356
                                                                                                                                                                                                                                                                                                                                                                                                                                                               GPKGSPGEAGRPGEAGLPGAKGLTGSPGSPGPDGKTGPPGPAGQDGRPGPPGPPGARGQA 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GVMGFPGPKGAAGEPGKAGERGVPGPPGAVGPAGKDGEAGAQGPPGPAGPAGERGEQGPA 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              417 GVMGFPGPKGAAGEPGKAGERGVPGPPGAVGPAGKDGEAGAQGPPGPAGPAGERGEQGPA 476
                                                                                                                                          A fusion protein (AAR89469) comprises the alpha-helical region of human collagen I(a) linked to the human mature bone morphogenic protein 2B (BMP2B). It can be expressed in Escherichia coli transformants carrying evector incorporating a chimeric gene (AAT16515) coding for the fusion. The BMP moiety induces osteogenesis, while the collagen moiety provides an integral substratum or scaffolding for the BMP and cells involved in reconstruction and growth. The fusion protein provides sustained release and delivery of BMP to a target tissue
                                                                                                                                                                                                                                                                                                                                                                                                  48
                                                                                                                                                                                                                                                                                                                                                                                                1 GPP------GEPGPTGLPGPPGERGGPGSRGFPGADGVAGPKGPAGERGSPGPA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Amino acid sequence of a chimeric collagen 1 (alphal)/BMP-2B protein.
                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ľ
                                                                                                                                                                                                                                                                                                                               Length 1169;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   note= "unspecified amino acid encoded by
                                                                                                                                                                                                                                                                                                                                                                2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    'note= "unspecified amino acid encoded
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GSPGFQGLPGPAGPPGEAGKPGEQGVPGDLGAPGPSGPAG 208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GSPGFQGLPGPAGPPGEAGKPGEQGVPGDLGAPGPSGARG
                                                                                                                                                                                                                                                                                                                                 DB 2;
                                                                                                                                                                                                                                                                                                                             Score 1149; DB 2
Pred. No. 7e-67;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     note= "Ala encoded by G"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAY84537 standard; protein; 1169
                                                                                                                English
                                                                                                                                                                                                                                                                                                                             97.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        99EP-00119184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                Matches 206; Conservative
                                                                                                                Disclosure; Fig 5; 59pp;
WPI; 1996-140144/15.
N-PSDB; AAT16515.
                                                                                                                                                                                                                                                                                                                                                 Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      890
                                                                                                                                                                                                                                                                                                   Sequence 1169 AA;
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Unidentified
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Best Local S
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The specification describes a method for producing an extracellular matrix protein or its fragment. The extracellular matrix protein is capable of self aggregating in a cell which does not ordinarily hydroxylated prolines. The method comprises optimising a nucleic acid equence for expression in the cell by substitution of codons preferred by that cell for naturally occurring codons not preferred by the cell; in corporating the nucleic acid sequence into the cell; and contacting the cell with a hypertonic growth medium containing at least one amino acid, selected from the group consisting of trans-4-hydroxyproline and 3-hydroxyproline to allow at least one of the amino acids to be assimilated into the cell and incorporated into the extracellular matrix protein. The method may be used to make host cells assimilate and incorporate trans-4-hydroxyproline into proteins. This is especially useful in the recombinant production of proteins such as collagen, fibrinogen and fibronectin whose ability to self aggregate and produce functional proteins depends on the post translational hydroxylation of proteins centod is also useful in studying the structure and function of proteins collagent (applat) (bone of the annual trans-4-hydroxyproline) or the post translational hydroxyproline. The present sequence represents a chimaric collagen (applat) (bone or the post collagen) (applat) (applat)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                morphogenic protein-2B (bmp-2b) protein, which may be produced using the method of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   297 GPPGPAGEEGKRGARGEPGPTGLPGPPGERGGPGSRGFPGADGVAGPKGPAGERGSPGPA
                                                                                                                                                                                                                                               Production of extracellular matrix proteins containing 4-trans-
hydroxyproline results in native self aggregating proteins, useful on
medical implants.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   12;
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Pred. No. 7e-67;
0; Mismatches 2; Indels 12;
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                                                                                                                                                                                                                                                                                                                                                                     Claim 22; Fig 13; 260pp; English.
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Best Local Similarity 93.6%;
Matches 206; Conservative
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Synthetic

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Chimaeric DNA encoding protein contg. extracellular matrix protein domain - and cellular regulatory factor domain, partic. useful as osteogenic agents, also related vectors, transformed cells and chimaeric proteins.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A fusion protein (AAR89470) comprises the alpha-helical region of human collagen I(a) linked to the human mature transforming growth factor beta-(1) if can be expressed in Escherichia coll transformants carrying a vector incorporating a chimeric gene (AAT16516) coding for the fusion. The TGF-beta- moiety increases efficacy of the body's normal soft tissue repair response and also induces osteogenesis. The collagen moiety provides an integral substratum or scaffolding for the TGF and cells involved in reconstruction and growth. The fusion protein provides sustained release and delivery of TGF-beta-1 to a target tissue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              297 GPPGPAGEEGKRGARGEPGPTGLPGPPGERGGPGSRGFPGADGVAGPKGPAGERGSPGPA 356
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                                                         1. .1057
/label= Collagen-IA
/note= "collagen IA alpha-helical domain"
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                                                                                                                                                                                                                                 "human mature TFF-beta-1"
                                                                                                                        /note= "unidentified amino acid"
                                                                                                                                                      'note≈ "unidentified amino acid"
                                                                                                                                                                   1058. .1059
/label= Linker_peptide
                                              Location/Qualifiers
                                                                                                                                                                                                 1060. .1171
/label= TGF-beta-1
/note= "human matu:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure; Fig 6; 59pp; English
                                                                                                                                                                                                                                                                                                                              95CA-02151547
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                                                                                                                                                                                                                                                                                                                                                                                                                         Espino P;
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     N-PSDB; AAT16516
                                                                                                        Misc-difference
                                                                                                                                      Misc-difference
                                                                                                                                                                                                                                                                                                                              12-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                           10-JUN-1994;
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                                                                                                                                                                     Peptide
                                              Key
Domain
                                                                                                                                                                                                   Domain
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AAY84538
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The specification describes a method for producing an extracellular matrix protein or its fragment. The extracellular matrix protein is capable of self aggregating in a cell which does not ordinarily hydroxylated prolines. The method comprises optimising a nucleic acid sequence for expression in the cell by substitution of codons preferred by the cell; on corporating the nucleic acid sequence into the cell; and contacting the incorporating the nucleic acid sequence into the cell; and contacting the cell with a hypertonic growth medium containing at least one amino acid, selected from the group consisting of trans-4-hydroxyproline and 3-chydroxyproline and along the cell and incorporated into the extracellular matrix protein. The method may be used to make host cells assimilate and incorporate trans-4-hydroxyproline into proteins. This is especially useful in the recombinant production of proteins such as collagen, fibrinogen and proteins depends on the post translational hydroxylation of proteins. The method is also useful in studying the structure and function of proteins component method is also useful in studying the structure and function of proteins depended to not normally contain trans-4-hydroxyprolline. The present sequence represents chimeric collagen 1 (alphal/transforming the present sequence represents chimeric collagen 1 (alphal/transforming the collagen by the cells of the collagen in the produced using the collagen in the collagen in the produced using the
                                                                                                                                                       Extracellular matrix protein; self aggregation; hydroxylated proline; trans-4-hydroxyproline; 3-hydroxyproline; recombinant protein production; collagen; fibrinogen; fibronectin; post translational hydroxylation; ss. transforming growth factor-betal; TGF-betal; chimera.
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hydroxyproline results in native self aggregating proteins, useful on
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GPP------GEPGPTGLPGPPGERGGPGSRGFPGADGVAGPKGPAGERGSPGPA
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                                                                                                                   A chimeric collagen 1 (alpha1)/TGF-betal protein.
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; Pred. No. 7e-67
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                            /note= "Gly encoded by GCT"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Zhang G,
AAY84538 standard; protein; 1171 AA
                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 23; Fig 15; 260pp; English.
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                                                                             25-JUL-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gruskin EA, Buechter DD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 93.6
Matches 206; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               N-PSDB; AAA12498.
                                                                                                                                                                                                                                                                                                                                                         Misc-difference
                                                                                                                                                                                                                                                          Homo sapiens
Unidentified
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      09-OCT-1998;
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                                     AAY84538;
                                                                                                                                                                                                                                                                                                Chimeric.
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297

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Gaps

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This invention relates to novel nucleic acids and proteins present in normal and neoplastic pancreatic cells. Pancreatic cancer is a common cause of cancer death worldwide, therefore accurate methods of diagnosis and treatment are required. Compounds which modulate the proteins of the invention may have cytostatic activity and the protein and DNA sequences of the invention may be useful for the development of a vaccine or in gene therapy. The composition and methods are useful in diagnosing, staging, imaging, monitoring, preventing or treating pancreatic cancer and non-cancercous disease states of the pancreas. The present sequence is that of a human pancreatic protein of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New pancreatic specific nucleic acid molecule or protein for diagnosing, staging, imaging, monitoring, preventing or treating pancreatic cancer or non-cancerous disease states of the pancreas.
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518 GPKGSPGEAGRPGEAGLPGAKGLTGSPGSPGPDGKTGPPGPAGQDGRPGPPGPPGARGQA
                                                                                                                        578 GVMGFPGPKGAAGEPGKAGERGVPGPPGAVGPAGKDGEAGAQGPPGPAGPAGERGEQGPA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            neoplastic pancreatic cell, pancreatic cell, pancreatic cancer, cancer death, cytostatic, vaccine, gene therapy, non-cancerous pancreas disease, human.
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                                                                                                                                                                            169 GSPGFQGLPGPAGPPGEAGKPGEQGVPGDLGAPGPSGPAG 208
                                                                                                                                                                                                                           638 dsperodipepharparackackegoveconcapepseare 677
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human pancreatic cell protein sequence SeqID522.
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                                                                                                                                                                                                                                                                                                                                                   ADE87062 standard; protein; 1226 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                    ADE87062;
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                                                                                                                                                                                                                                                                                                      RESULT 15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                49 GPKGSPGEAGRPGEAGLPGAKGLTGSPGSPGPDGKTGPPGPAGQDGRPGPPGPPGARGQA 108
                               GPKGSPGEAGRPGEAGLPGAKGLTGSPGSPGPDGKTGPPGPAGQDGRPGPPGPPGARGQA 108
                                                                           357 GPKGSPGEAGRPGEAGLPGAKGLTGSPGSPGPDGKTGPPGPAGQDGRPGPPGPPGARGQA 416
                                                                                                                             GVMGFPGPKGAAGEPGKAGERGVPGPPGAVGPAGKDGEAGAQGPPGPAGPAGERGEQGPA 168
                                                                                                                                                                         GVMGFPGPKGAAGEPGKAGERGVPGPPGAVGPAGKDGEAGAQGPPGPAGPAGERGEQGPA 476
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This invention relates to novel nucleic acids and proteins present in normal and neoplastic pancreatic cells. Pancreatic cancer is a common cause of cancer death worldwide, therefore accurate methods of diagnosis and treatment are required. Compounds which modulate the proteins of the invention may have cytostatic activity and the protein and DNA sequences of the invention may be useful for the development of a vaccine or in gene therapy. The composition and methods are useful in diagnosing, staging, imaging, monitoring, preventing or treating pancreatic cancer and non-cancerous disease states of the pancreas. The present sequence is that of a human pancreatic protein of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 GPP-----GEPGPTGLPGPPGERGGPGSRGFPGADGVAGPKGPAGERGSPGPA 48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New pancreatic specific nucleic acid molecule or protein for diagnosing, staging, imaging, monitoring, preventing or treating pancreatic cancer conn-cancerous disease states of the pancreas.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              neoplastic pancreatic cell; pancreatic cell; pancreatic cancer; cancer death; cytostatic; vaccine; gene therapy; non-cancerous pancreas disease; human.
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                                                                                                                                                                                                                             GSPGFQGLPGPAGPPGEAGKPGEQGVPGDLGAPGPSGPAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human pancreatic cell protein sequence SeqID517.
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                                                                                                                                                                                                                                                                                                                                                                                                  ADE87057 standard; protein; 1211
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N-PSDB; ADE87397.
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169 GSPGFQGLPGPAGPPGBAGKPGEQGVPGDLGAPGPSGPAG 208
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Search completed: September 24, 2004, 11:09:14 Job time : 31.5883 secs

GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd.

(without alignments) 2603.588 Million cell updates/sec September 24, 2004, 11:07:31; Search time 67.1873 Seconds 1 GSEGPEGVRGEPGPPGPAGA.......PGPSGDAGPPGPPGPAGKEG 544 - protein search, using sw model US-10-658-989A-4 3070 Title: Perfect score: OM protein Sequence: Run on:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

1349238 segs, 321558718 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Published Applications AA:*

1: \cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*
2: \cgn2_6/ptodata/1/pubpaa/PCT_MEW_PUB.pep:*
3: \cgn2_6/ptodata/1/pubpaa/PCT_MEW_PUB.pep:*
4: \cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*
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8: \cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
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18: \cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*
18: \cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

					SUMMARIES	
		ф				
Result	,	Query	Query			
	Score	Match	Length	DB	QI	Description
н	2966	96.6	1057	16	US-10-104-889-16	Sequence 16, Appl
N	2966	96.6	1057	16	US-10-104-889-20	Sequence 20, Appl
m	2966	9.96	1107	16	US-10-104-889-11	Sequence 11, Appl
4	2966	96.6	1169	16	US-10-104-889-6	6, A
2	2966	96.6	1171	16	US-10-104-889-8	80
9	2966	96.6	1388	16	US-10-104-889-10	10,
7	2966	96.6	1461	16	US-10-468-091-25	25,
80	2966	96.6	1464	12	US-09-918-715-261	
o,	2966	96.6	1464	14	US-10-060-036-159	Sequence 159, App
10	2966	96.6	1464	14	US-10-171-311-36	Sequence 36, Appl
11	2966	96.6	1464	74	US-10-216-705-21	Sequence 21, Appl
12	2966	96.6	1464	14	US-10-149-352-2	2, 4
13	2966	96.6	1464	14	US-10-177-293-65	65
14	2966	96.6	1464	14	US-10-301-822-28	Sequence 28, Appl
15	2966	9.96	1464	15	US-10-291-265-243	243,

1000	Appli	Appli	Appl	Appli	Appli	Appl	Appl	Appli	Appli	, Appl	Appl	Appli	Appl	Appli	Appl	Appli	Appl	Appl	Appl	Appl	Appl	App1	Appl	Appl	Appl	App1	App1	Appl	Appl	Appli
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ALIGNMENTS

COMPUTRY: U.S.A.

ZIP: 11553

COMPUTER: READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: BM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/104,889
FILING DATE: 22-Mar-2002
CLASSIFICATION: <UNKNOWN>
PRIOR APPLICATION: <UNKNOWN>
PRIOR SPELICATION DATA:
APPLICATION NUMBER: US/09/169,768
FILING DATE: 09-OCT-1998
APTORNEY/AGENT INFORMATION:
TELEPHONE: (516) 228-8484
TELEPHONE: (516) 228-8484
TELEFAX: (516) 228-8516
; INFORMATION FOR SEG ID NO: 16:
SEQUENCE CHARACTERISTICS: RESULT 1
US-10-104-889-16
Sequence 16, Application US/10104889
Sequence 16, Application US/10104889
Publication No. US20040086561A1
GENERAL INFORMATION:
BUCKHAR, DOUGHAS
BROCKAW, JANE
TITLE OF INVENTION: AMINO ACID MODIFIED POLYPEPTIDES
NUMBER OF SEQUENCES: 50
CORRESPONDENCES: DIMORTH & BARRESE
STREET: 333 EARLE OVINGTON BOULEVARD
CITY: UNDAALE
STATE: NY

15-10-000-000-1-st

Sep 24 11:45:39 2004

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GPPGAVGPAGKDGEAGAQGPPGPAGPAGERGEQGPAGSPGFQGLPGPAGPPGEAGKPGEQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  321 GPPGERGGPGSRGFPGADGVAGPKGPAGERGSPGPAGPKGSPGEAGRPGEAGLPGAKGLT
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            CORDUTE: TALPA USING TALLA COMPUTE: TALPA USING SYSTEM: PC COMPATIBLE OFFICE OF
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96.6%; Score 2966; DB 16;
Best Local Similarity 95.6%; Pred. No. 4.9e-146;
Matches 520; Conservative 21; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: amino acid
STRANDEDNESS: single
STRANDEDNESS: single
TOPOLOGY: unknown
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 20:
                                                                                                                                                                                                                                                                                                                                                                                             TELEPHONE: (516) 228-8484
TELEFAX: (516) 228-8516
                                                                                                                                                                                                                                                                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 1057 amino acids
                                                                                                                                                                                                                                                                                                                                          NAME: STEEN, JEFFREY S
TELECOMMUNICATION INFORMATION
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US-10-104-889-11
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Publication No. US20040086561A1
GENERAL INFORMATION:
BUBCHIER, DOUGLAS
BROKAM, JANE
ZHANG, GUANGHUI
PROLELLA, DAVID
TITLE OF INVENTION: AMINO ACID MODIFIED POLYPEPTIDES
NUMBER OF SEQUENCES: 50
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                                                                                                                                                                                                                        96.6%; Score 2966; DB 16; 95.6%; Pred. No. 4.9e-146; tive 21; Mismatches 3;
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ADDRESSE: DILWORTH & BARRESE
STREET: 333 EARLE OVINGTON BOULEVARD
CITY: NUTONDALE
STATE: NY
                     TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: unknown
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 16:
US-10-104-889-16
SENGTH: 1057 amino acids
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Matches 520;
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APPLICATION NUMBER: US/09/169,768
FILING DATE: 09-0CT-1998
ATTORNEY/AGENT INFORMATION:
NAME: STEEN, JEFFREY S
TELECOMMUNICATION: STRANBEDNESS: single
STRANBEDNESS: single
TOPOLOGY: unknown
NOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-10-104-889-6 TELEPHONE: (516) 228-8484 TELEFAX: (516) 228-8516 LENGTH: 1169 amino acids g ò

201 GSEGPQGVRGEPGPPGPAGAAGPAGNPGADGQPGAKGANGAPGIACAPGFAGARGPSGPQ 260

1 GSEGPEGVRGEPGPPGPAGAAGPAGDPGADGEPGAKGADGAPGIAGAPGFPGARGPSGPE

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Ouery Match 96.6%; Score 2966; DB 16; Best Local Similarity 95.6%; Pred. No. 5.1e-146; Matches 520; Conservative 21; Mismatches 3;

Length 1107;

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321 GPPGERGGPGSRGFPGADGVAGPKGPAGERGSPGPAGPKGSPGEAGRPGEAGLPGAKGLT 380

121 GPPGERGGPGSRGFPGADGVAGPKGPAGERGSPGPAGPKGSPGEAGRPGEAGLPGAKGLT 180

GSPGSPGRDGKTGPPGPAGQDGRPGPPGPPGAKGQAGVMGFPGFKGAAGEPGKKAAGVVV 440

GSPGSPGPDGKTGPPGPAGEDGRPGPPGPPGARGEAGVMGFPGPKGAAGEPGKAGERGVP 240

181 381 241 GVPGDLGAPGPSGARGEPGERGVEGPPGPPGPAGPGADGARGDAGAGGAPGAPGS 360

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GPPGAVGPAGKDGEAGAEGPPGPAGPAGERGEEGPAGSPGFEGLPGPAGPPGEAGKPGEE 300

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BROKAM, JANBE
ZHANG, GUANGHUI
PAOLELLA, DAVID
TITLE OF INVENTION: AMINO ACID MODIFIED POLYPEPTIDES
NUMBER OF SEQUENCES: 50
CORRESPONDENCE ADDRESS:
                                                                                                                          96.6%; Score 2966; DB 16; 95.6%; Pred. No. 5.4e-146; iive 21; Mismatches 3;
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STREET: 333 EARLE OVINGTON BOULEVARD
CITY: UNIONDALE
STRANDEDNESS: single
STRANDEDNESS: single
TOPOLOGY: unknown
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 8:
US-10-104-889-8
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US-10-104-889-10
Sequence 10, Application US/10104889
Publication No. US20040086961A1
GENERAL INFORMATION:
APPLICANT: GRUSKIN, ELLIOT A.
BUECHTER.
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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                                          GPPGERGGPGSRGFPGADGVAGPKGPAGERGSPGPAGPKGSPGEAGRPGEAGLPGAKGLT
                                                                                       GSPGSPGPDGKTGPPGPAGEDGRPGPPGPPGARGEAGVMGFPGPKGAAGEPGKAGERGVP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: AMONGTON MODIFIED POLYPEPTIDES
NUMBER OF SEQUENCES: 50
CORRESPONDENCE SIGN
STREET: 33 BARLE OVINGTON BOULEVARD
STREET: NUMBER OVINGTON BOULEVARD
STREET: NUMBER OVINGTON BOULEVARD
STREET: NUMBER OVINGTON BOULEVARD
STATE: NY
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COMPUTER READABLE FORM:
MEDIUM TYPE: Rloppy disk
COMPUTER: LBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Ver
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/104,889
FILING DATE: 22-Mar-2002
CLASSIFICATION: «Unknown»
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/169,768
FILING DATE: 09-0CT-1998
ATTORNEY/AGENT INFORMATION:
NAME: STEEN, USFREY S
TELECOMMUNICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEPHONE: (516) 228-8484
TELEFAX: (516) 228-8516
INFORMATION FOR SEG ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 1171 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 8, Application US/10104889
Publication No. US20040086961A1
GENERAL INFORMATION:
APPLICANT: GRUSKIN, ELLIOT A.
BUECHTER, DOUGLAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY: U.S.A.
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publication No. US20040157329A1

j GRURRAL INFORMATION:
   APPLICANT: ADP Pharmaccutical Pty Limited
   APPLICANT: The University of Sydney
   TITLE OF INVENTION: Matrix gene expression in chondrogenesis
   FILE REFERENCE: 50031018R: US/10/468,091
   CURRENT APPLICATION NUMBER: US/10/468,091
   CURRENT FILING DATE: 2003-08-13
   PRIOR APPLICATION NUMBER: AU PR3116
   PRIOR PRILING DATE: 2001-02-15
   NUMBER OF SEQ ID NOS: 42
   SOFTWARE: Patentin version 3.1
   SEQ ID NO 25

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 96.6%; Score 2966; DB 16; Length 1461; Best Local Similarity 95.6%; Pred. No. 6.4e-146; Matches 520; Conservative 21; Mismatches 3; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT
CORGANISM: Homo sapiens
US-10-468-091-25
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96.6%; Score 2966; DB 16; Length 1388;
Best Local Similarity 95.6%; Pred. No. 6.1e-146;
Matches 520; Conservative 21; Mismatches 3; Indels 0;
         COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/104,889
FILING DATE: 22-Mar-2002
CLASSIFICATION: <unvented to the company of the compan
                                                                                                                                                                                                     PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/169,768
FILING DATE: 09-0CT-1998
ATTORNEY AGENT INFORMATION:
NAME: STEEN, JEFFREY S
TELECOMMONICATION INFORMATION:
TELEPHONE: (516) 228-8484
TELEFAX: (516) 228-8516
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: unknown
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 10:
US-10-104-889-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
LENGTH: 1388 amino acids
TYPE: amino acid
STRANDEDNESS: single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               779 GESGPSGPAGPTGARGAPGDRGEPGPPGPAGPAGPPGADGQPGAKGEPGDAGARGDAGPP
                                                                                                                                                   GPGGPPGPKGDSGEPGAPGSKGDTGAKGEPGPVGVEGPPGPAGEEGKPGARGEPGPTGLP
                                                                                                                                                                                             419 GPGGPPGPKGNSGEPGAPGSKGDTGAKGEPGPVGVQGPPGPPGPAGEEGKRGARGEPGPTGLP
                                                                                                                                                                                                                                                      GPPGERGGPGSRGFPGADGVAGPKGPAGERGSPGPAGPKGSPGEAGRPGEAGLPGAKGLT
                                                                                                                                                                                                                                                                                   479 GPPGERGGPGSRGFPGADGVAGPKGPAGERGSPGFPAGPKGSPGEAGRPGEAGLPGAKGLT
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                                                     1 GSEGPEGVRGEPGPPGPAGAAGPAGDPGADGEPGAKGADGAPGIAGAPGFPGARGPSGPE
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Gaps
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Publication No. US20030017157A1
GENERAL INFORMATION:
APPLICANT: Berd St. Croix
APPLICANT: Remach Kanzler
TITLE OF INVENTION: ENDOTHELIAL CELL EXPRESSION PATTERNS
FILE REFERENCE: 1107.00134
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RESULT 7 US-10-468-091-25 ; Sequence 25, Application US/10468091

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Gaps .; 0 421

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481 180 601 300 360

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GAPGLEGMPGERGAAGLPGPKGDRGDAGPKGADGSPGKDGVRGLTGPIGPPGPAGAPGDK 420
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Sequence 36, Application US/10171311

GENERAL INFORMATION:

APPLICANT: Schlegel, Robert

APPLICANT: Chen, Yan

APPLICANT: Chen, Yan

APPLICANT: Kamatkar, Shubhangi

APPLICANT: Gannavarapu, Man

APPLICANT: Gannavarapu, Manjula

APPLICANT: Hoersh, Sebastian

APPLICANT: Hoersh, Sebastian

APPLICANT: IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY

TITLE OF INVENTION: OF CERVICAL CANCER
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          AND DIAGNOSIS OF PANCREATIC CANCER
                                                                                                                                                                                                                                                  Query Match 96.6%; Score 2966; DB 14; Best Local Similarity 95.6%; Pred. No. 6.4e-146; Matches 520; Conservative 21; Mismatches 3;
                       FILE REFERENCE: 210121.56
CURRENT APPLICATION NUMBER: US/10/060,036
CURRENT FILING DATE: 2002-01-30
NUMBER OF SEQ ID NOS: 4560
SOFTWARE: SESLED for Windows Version 4.0
SEQ ID NO 159
LENGTH: 1464
                                                                                                                                                                                      ; ORGANISM: Homo sapiens
US-10-060-036-159
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US-10-060-036-159
US-10-060-036-159
Sequence 159, Application US/10060036
Publication No. US20030073144A1
GENERAL INFORMATION:
APPLICANT: Relson, Darin R.
APPLICANT: Lodes, Michael D.
APPLICANT: Persing, David H.
APPLICANT: Hepler, William T.
APPLICANT: Hepler, William T.
APPLICANT: Jiang, Yuqiu
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                96.6%; Score 2966; DB 12;
95.6%; Pred. No. 6.4e-146;
tive 21; Mismatches 3;
CURRENT APPLICATION NUMBER: US/09/918,715
CURRENT FILING DATE: 2001-08-01
PRIOR PEDLICATION NUMBER: 60/222,599
PRIOR PELING DATE: 2000-08-02
PRIOR APPLICATION NUMBER: 60/224,360
PRIOR PELING DATE: 2000-08-11
PRIOR APPLICATION NUMBER: 60/282,850
PRIOR PELING DATE: 2000-04-11
PRIOR APPLICATION NUMBER: 60/282,850
PRIOR FILING DATE: 2000-04-11
PRIOR PELING DATE: 2000-04-11
PRIOR PELING DATE: 2000-04-11
PRIOR PELING DATE: 2000-04-11
                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 95.6%
Matches 520; Conservative
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| LENGTH: 1464
| TYPE: PRT
| ORGANISM: Homo sapiens
| US-09-918-715-261
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95.6%; Pred. No. 6.4e-146;
ive 21; Mismatches 3;
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US-10-149-352-2
Sequence 2. Application US/10149352
Sequence 2. Application US/10149352
Publication No. US2030105050A1
GENERAL INFORMATION:
TITLE OF INVENTION: ANTISENSE OLIGONUCLEOTIDES
FILE REFERENCE: 06275-254US1
CURRENT FILING DATE: 2002-06-10
PRIOR PILING DATE: 2002-06-10
PRIOR PILING DATE: 2000-12-12
PRIOR PILING DATE: 1999-12-15
NUMBER OF SEQ ID NOS: 14
SEQ ID NO 2
LENGTH: 1464
PRIOR APPLICATION NUMBER: US 09/331,347
PRIOR FILING DATE: 1999-08-17
NUMBER OF SEQ ID NOS: 22
SOFTWARE: Patentin version 3.1
SEQ ID NO 21
LENGTH: 1464
TYPE: PRT
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                                                                                                                                    ; ORGANISM: Homo sapiens
US-10-216-705-21
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Publication No. US20030096973A1
GENERAL INFORMATION:
APPLICATION Meristem Therapeutics, S.A.
TITLE OF INVENTION: Recombinant Collagens and ITILE OF INVENTION: obtaining Such and Their IFILE REPRENCE: 1149-3 DIV
CURRENT APPLICATION NUMBER: US/10/216,705
CURRENT FILING DATE: 2002-08-09
FILE REFERENCE: MRI-035
CURRENT APPLICATION NUMBER: US/10/171,311
CURRENT PILING DATE: 2002-06-12
FRIOR APPLICATION NUMBER: US 60/298,159
PRIOR FILING DATE: 2001-06-13
PRIOR FILING DATE: 2001-06-13
PRIOR FILING DATE: 2001-06-13
PRIOR FILING DATE: 2001-06-13
PRIOR FILING DATE: 2001-11-14
NUMBER OF SEQ ID NOS: 238
SOFTWARE: FRALESEQ FOR Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 95.6
Matches 520; Conservative
                                                                                                                                                                                                                                                       TYPE: PRT
CORGANISM: Homo sapiens
US-10-171-311-36
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US-10-216-705-21
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Best Local Similarity 95.6%; Pred. No. 6.4e-146;
Matches 520; Conservative 21; Mismatches 3;
    PREVENTION, AND THERAPY OF
                     FILE REFERENCE: MRI-038

CURRENT APPLICATION NUMBER: US/10/177,293

CURRENT FILING DATE: 2002-06-21

PRIOR APPLICATION NUMBER: US 60/299,887

PRIOR FILING DATE: 2001-06-21

PRIOR FILING DATE: 2001-06-27

PRIOR FILING DATE: 2001-06-27

PRIOR FILING DATE: 2001-06-27

PRIOR PILING DATE: 2001-06-27

PRIOR PILING DATE: 2001-09-25

PRIOR FILING DATE: 2001-09-25

PRIOR FILING DATE: 2001-09-25

PRIOR FILING DATE: 2002-05

PRIOR FILING DATE: 2002-05

PRIOR FILING DATE: 2002-05

PRIOR FILING DATE: 2002-05

PRIOR FILING DATE: 2002-05-14

NUMBER OF SEQ ID NOS: 506

SEQ ID NOS: 506

SEQ ID NOS: 506
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US-10-177-293-65
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TYPE: PRT
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US-10-301-822-28
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APPLICANT: Mills, Gordon B.
TITLE OF INVENTION: COMPOSITIONS, KITS, AND METHODS FOR IDENTIFICATION, ASSESSMENT,
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Publication No. US20030124128A1
GENERAL INFORMATION:
APPLICANT: Lillie, James
APPLICANT: Glatt, Karen
APPLICANT: Gannavarpu, Manjula
APPLICANT: Ramatkar, Shubhangi
APPLICANT: Kamatkar, Shubhangi
APPLICANT: Wertens, Maureen
APPLICANT: Wang, Youzhen
APPLICANT: Wang, John
APPLICANT: Monahan, John
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Xu, Yongyao
Hoersch, Sebastian
Monahan, John
Meyers, Rachel E.
Bast Jr., Robert C.
Hortobagyi, Gabriel N
Pusztai, Lajos
Meric, Funda
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-149-352-2
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Best Local S
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Best Local Similarity 95.6
Matches 520; Conservative
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CORGANISM: Homo sapiens
US-10-291-265-243
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                                    APPLICANT: Berger, Allison
APPLICANT: Berger, Allison
APPLICANT: Guillemette, Tracy L.
APPLICANT: Guillemette, Tracy L.
APPLICANT: Schlegel, Robert
APPLICANT: Schlegel, Robert
APPLICANT: Schlegel, Robert
APPLICANT: Thibodeau, Stephen N.
APPLICANT: Thibodeau, Stephen N.
APPLICANT: Monahan, John E.
APPLICANT: Hawrence N.
TITLE OF INVENTION: THERAPO OF COLON CANCER
TITLE OF INVENTION NUMBER: US 60/339, 971
PRIOR APPLICATION NUMBER: US 60/381, 978
PRIOR PLING DATE: 2002-03-05
PRIOR FILING DATE: 2002-03-05
PRIOR PRIOR APPLICATION NUMBER: US 60/381, 988
PRIOR FILING DATE: 2002-03-05
PRIOR PLING DATE: 2002-03-05
PRIOR APPLICATION NUMBER: US 60/381, 988
PRIOR PLING DATE: 2002-03-05
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                         llennium Pharmaceuticals,
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CRGANISM: Homo Sapiens
US-10-301-822-28
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Best Local Similarity
Matches 520; Conserv
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SENERAL INFORMATION:
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WESULY 15
US-10-201-265-243
US-10-201-265-243
Sequence 243, Application US/10291265
Publication No. US20030232054A1
SEGNERAL INFORMATION:
APPLICANT: Hyseq. Inc.
APPLICANT: Tang et al
TITLE OF INVENTION: NO. US20030232054A1e1 Nucleic Acids and Polypeptides
FILE REFERENCE: 21272-017 (785)
CURRENT APPLICATION NUMBER: US/10/291,265
CURRENT APPLICATION NUMBER: US/404
PRIOR FILING DATE: 2000-01-25
PRIOR APPLICATION NUMBER: 09/491,404
PRIOR FILING DATE: 2000-07-17
PRIOR APPLICATION NUMBER: 09/617,746
PRIOR FILING DATE: 2000-09-05
PRIOR FILING DATE: 2000-09-05
NUMBER OF SEQ ID NOS: 944
SOFTWARE: FastSEQ for Windows Version 3.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            362 GSEGPQGVRGEPGPPGPPGPAGAAGPAGNPGADGQPGAKGANGAPGIAGAPGFPGARGPSGPQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     482 GPPGERGGPGSRGFPGADGVAGPKGPRGPRGSPGPAGPKGSPGEAGRPGBAGLT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      542 GSPGSPGPDGKTGPPGPAGQDGRPGPPGPPGARGQAGWMGFPGPKGAAGEPGKAGERGVP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          782 GESGPSGPAGPTGARGAPGDRGEPGPPGPAGFAGPPGADGQPGAKGEPGDAGAKGDAGPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 GSEGPEGVRGEPGPPGPAGAAGPAGDPGADGEPGAKGADGAPGIAGAPGPPGARGPSGPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 GPGGPPGPKGDSGEPGAPGSKGDTGAKGEPGPVGVEGPPGPAGEEGKPGARGEPGPTGLP
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Search completed: September 24, 2004, 11:13:25 Job time : 69.1873 secs

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GenCore version 5.1.6
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                  Copyright
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- protein search, using sw model OM protein

September 24, 2004, 11:06:56; Search time 20.9509 Seconds (without alignments) 2497.663 Million cell updates/sec Run on:

Title: Perfect score:

US-10-658-989A-4 3070 1 GSEGPEGVRGEPGPPGPAGA......PGPSGDAGPPGPPGKEG 544 Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283366 segs, 96191526 residues Searched:

Total number of hits satisfying chosen parameters:

length: 0 length: 200000000 DB seq DB seq Minimum I Maximum I

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

1: pirl: * 2: pirl: * 3: pir2: * 4: pir4: * PIR Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	lagen alpha 1	alpha 1	lagen alpha 1	lagen alpha 1	lagen alpha 1	collagen alpha 1(I	alpha 1	alpha 1	alpha 1	alpha 1	lpha 1	lpha 2	N	n type	lpha 1	lpha 1	lpha 1	lpha 2	lpha 1	lpha 2	alpha 1	collagen alpha 1(X	collagen alpha 1(V	alpha	alpha	lagei	lagen alpha	lagen alpha	collagen alpha 5(I
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collagen alpha 1(V	collagen alpha 2(I	type VII collagen	collagen alpha 4(I	collagen alpha 1(X	collagen alpha 3(I	collagen alpha 1 (V	collagen alpha 1(I	hypothetical prote	collagen alpha 1(I	collagen alpha 2(I	collagen COLF1 - f	collagen alpha 2(I	collagen alpha 5(I	collagen alpha 1(I	collagen alpha 1(X
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A548	S1636	148103	CGH01	S2381	CGHU3	A4574	CGHU41	T2935(CGMS4E	T2935	831521	CGHUZI	A55267	84261	TXD36
2 A548	2 81636	2 I4810	1 CGHU1	2 \$2381	1 CGHU3	2 A4574	1 CGHU41	2 T2935(1 CGMS4E	2 T2935	2 83152:	1 CGHUZI	2 A5526	2 84261	2 TX036
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44.8 2944 2	1763 2	44.4 1549 2	44.2 1690 1	43.6 1603 2	43.6 1670 1	43.5 920 2	43.0 1669 1	42.7 1758 2	42.7 1669 1	42.6 1759 2	42.5 812 2	41.9 1712 1	41.7 754 2	41.6 921 2	41.6 1142 2

ALIGNMENTS

_	RESULT 1
	CGHU1S
	collagen alpha 1(I) chain precursor - human
	N;Alternate names: procollagen alpha 1(I) chain
	C;Species: Homo sapiens (man)
	C;Date: 12-Aug-1981 #sequence revision 04-Oct-1996 #text change 31-Dec-2000
	C;Accession: I60114; S01143; A93335; I55254; A39943; I55237; A35233; S09400; B90567; S11
	5269; A29439; I53466; A02852; I37247
	R;D'Alessio, M.; Bernard, M.; Pretorius, P.J.; de Wet, W.; Ramirez, F.; Pretorious, P.J.
_	Gene 67, 105-115, 1988
	A, Title: Complete nucleotide sequence of the region encompassing the first twenty-five e.
	A; Reference number: 160114; MUID: 88329734; PMID: 2843432
-	A; Accession: 160114

translated from GB/EMBL/DDBJ

Aymolecule type: DNA

Aymolecule type: BNA

A;Reference number: 155254; MUID:88033098; PMID:2822714

A;Status: translation not shown; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-45 - KROS
A;Cross-references: GB:JC2829; NID:g180387; PIDN:AAA51993.1; PID:g180388
B;Bornstein, P.; McKay, J.; Morishima, J.K.; Devarayalu, S.; Gelinas, R.E.
Proc. Natl. Acad. Sci. U.S.A. 84, 8869-8873, 1987
A;Title: Regulatory elements in the first intron contribute to transcriptional control on A;Reference number: A39943; MUID:88097389; PMID:3480516
A;Accession: A39943

A,Molecule type: DNA A,Residues: 1-34 RBOR> A,Cross-references: GB:J03559; NID:g180876; PIDN:AAA52052.1; PID:g553238 R;Chu, M.L.; de Wet, W.; Bernard, M.; Ramirez, F.

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A, Molecule type: mRNA
A, Residues: 342-352, 'C', 354-359 <WI2>
A, Residues: 342-352, 'C', 354-359 <WI2>
A, Cross-references: GB:S64717, NID:9408195, PIDN:AAB27677.1; PID:9408196
A, Note: mutant sequence from patient with osteogenesis imperfects
R, Bernard, M. P.; Chu, M. L.; Myers, J. C.; Ramirez, F.; Eikenberry, E.F.; Prockop, D.J.
B, Chellery 22, 5213-5223, 1983
A, Title: Nucleotide sequences of complementary deoxyribonucleic acids for the proalphal of A, Reference number: A90476; MUID:84080385; PMID:6689127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Molecule type: mRNA
A; Residues: 425-1250, Xr, 1252-1328, Sr, 1330-1390, Xr, 1392-1464 < BER>
A; Cross-references: GB: K01228, NID: g180391; PIDN: AAA51995.1; PID: g180392
A; Note: sequence partially completed for missing nucleotides by A29439
R; Chu, M.L.; Gargiulo, V.; Williams, C.J.; Ramirez, F.
A; Blol. Chem. 260, 691-694, 1985
A; Title: Multiaxon deletion in an osteogenesis imperfecta variant with increased type III
A; Reference number: A22161; MUD: 85104934; PMID: 2981843
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Molecule type: mRNA
A;Residues: 1179-1276, H',1278-1336,1339-1387, R',1389-1464 <CHE>
A;Cross-references: GB:S64596; NID:g407589; PIDN:AAB27856.1; PID:g407590
A;Note: sequence extracted from NCBI backbone (NOBIN:136444, NCBIP:136445)
A;Note: does not represent an experimentally determined sequence but three different muts
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R; Cohn, D.H.; Apone, S.; Eyre, D.R.; Starman, B.J.; Andreassen, P.; Charbonneau, H.; Nich
R; Cohn, Chem. 263, 14605-14607, 1988
A; Title: Substitution of Cysteine for Glycine within the Carboxyl-terminal Telopeptide of
A; Reference number: 155269; MUID:89008319; PMID:3170557
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A,Molecule type: DNA
A,Residues: 472-594, R.,596-607 <CH3>
A,Residues: 472-594, R.,596-607 <CH3>
A,Cross-references: GB:KO3178; GB:KO3179; NID:g179612; NID:g179613; PIDN:AAA51847.1; PID:
A,Note: the authors translated the codon CGT for residue 595 as Pro
A,Note: the authors translated the codon CGT for residue 595 as Pro
A;Nallis: Q.A.; Starman, B.J.; Zinn, A.B.; Byers, P.H.
Am. J. Hum. Genet. 46, 1034-1040, 1990
A;Title: Variable expression of osteogenesis imperfecta in a nuclear family is explained
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Modecule type: mRNA
A; Residues: 710-720, E',722-737, E',739-745 < WAL>
A; Residues: 710-720, E',722-737, E', 739-745 < WAL>
A; Note: the authors translated the codons CAG for 721 and CGT for 738 as Glu
A; Note: the authors translated the codons CAG for 721 and CGT for 738 as Glu
R; Forlino, A.; Zolezzi, F.; Valli, M.; Pignatti, P.F.; Cetta, G.; Brunelli, P.C.; Mottes,
Hum. Mol. Genet. 3, 2201-2206, 1994
Hymm. Mol. Genet. 3, 2201-2206, 1994
A; Title: Severe (type III) osteogenesis imperfecta due to glycine substitutions in the Cf
A; Reference number: IS4365, MUID:95187161; PMID:7881420
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AjMolecule type: DNA
AjRediues: T46-766, %7 768-781 AFORA
AjRediues: 746-766, %7 768-781 AFORA
AjRediues: 746-766, %7 768-781 AFORA
Ajrediues: 748-766, %7 768-781 AFORA
Ajrediues: 748-766, %7 81115, %7 81115, %7 81115, %7 8118-1825, 1939
Ajritle: Mutations in the carboxyl-terminal propeptide of the pro alpha 1(1) chain of Ajredium number: A47426, MUID:93352646, PMID:8349697
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Reference number: A35336; MUID:90252792; PMID:2339700
A;Accession: A35336
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A; Residues: 1179-1387, 'R', 1389-1464 <CH7>
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A;Residues: 1179-1276,'H',1278-1464 <CH5>
A;Residues: 1179-1276,'Experimental source: fetal cell 86-237
A;Accession: D47426
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A;Residues: 1179-1336,1339-1464 <CH6>
A;Residues: 1179-1336,1339-1464 <CH6
A;Accession: Et7426
A;Accession: E47426
                A;Accession: I52905
A;Status: translated from GB/EMBL/DDBJ
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Residues: 1179-1464
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A; Molecule type: protein
A; Residues: 175-187; 274-287, P., 289 cBAE>
A; Residues: 175-187; 274-287, P., 289 cBAE>
A; Residues: 175-187; 274-287, P., 289 cBAE>
A; Molecule sequence of collagen alpha 1(S)(I) isolated from bone after pepsin digestion
A; Molecule: sequence of collagen alpha 1(S)(I) isolated from bone after pepsin digestion
A; Deak, S.B.; Scholz, P.M.; Amenca, P.S.; Constantinou, C.D.; Levi-Minzi, S.A.; Gonzalez
A; Diol. Chem. 266, 21827-21832, 1991
A; Title: The substitution of arginine for glycine 85 of the alpha 1(I) procollagen chain coperative melting of intact type I collagen.
A; Reference number: 155342; MUID:92042092; PMID:1718984
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A, Residues: 258-268;1347-1357 <DEA>
A, Residues: 258-268;1347-1357 <DEA>
A, Cross-references: GB:867495; NID:9239007; PIDN:AAB20350.1; PID:9239008
A, Note: sequences from the 5. and sonly are shown; mutant sequence 263-Arg report
R, Morgan, P. H.; Jacobs, H.G.; Segrest, J.P.; Cunningham, L.W.
J. Biol. Chem. 245, 5042-5048, 1970
A, Ritiles: Comparative study of glycopeptides derived from selected vertebrate collagens.
A, Reference number: A92069; MuID:71001508; PMID:4319110
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R;Wirtz, M.K.; Keene, D.R.; Hori, H.; Glanville, R.W.; Steinmann, B.; Rao, V.H.; Hollist
J. Biol. Chem. 265, 6312-6317, 1990
A;Tibol. Chem. 265, 6312-6313, MUID:90202908; PMID:2318855
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Note: this propeptide fragment remained non-covalently bound to a defective, uncleaved R;Weil, D.; d'Alessio, M.; Ramirez, F.; de Wet, W.; Cole, W.G.; Chan, D.; Bateman, J.F. EMBO J. 8, 1705-1710, 1989
A;Afference humber: Substitution in the exon of a collagen gene causes alternative splicing A;Reference number: S09400; MUID:8935643; PMID:2767050
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A,Molecule type: protein
A,FResidues: 162-198, 72',200-201, 2',203-206, 2',208-209, 2',211-228, B',230, BB',233, 2'
A,Experimental source: skin
A,Experimental source: skin
A,Dote: evidence for 10-allysine
R,Bactge, B.; Notbohm, H.; Diebold, J.; Lehmann, H.; Bodo, M.; Deutzmann, R.; Mueller, E Bur. J. Biochem. 192, 153-159, 1990
A,Title: A Critical crosslink region in human-bone-derived collagen type I. Specific cle
A,Reference number: S11372; MUID:90382436; PMID:2169412
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Molecule type: mRNA
A; Residues: 156-183 "WEI>
A; Residues: 156-184 "WEI>
B; Colick, BM; Bornstein, P.
Biochemistry 9, 4699-4706, 1970
A; Title: Isolation and characterization of the cyanogen bromide peptides from the alphal
A; Contents: CNBE0-1, CNBE2, CNBE4, CNBE5
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A,Residues: 281-302;402-420;823-843;925-944;1026-1045;1143-1162 <LAB>
R,Wirtz, M.K.; Rao, V.H.; Glanville, R.W.; Labhard, M.E.; Pretorius, P.J.; de Vries, W.N.
Connect. Tissue Res. 29, 1-11, 1933
A;Tille: A cysteine for glycine substitution at position 175 in an alpha 1 (I) chain of
A;Reference number: I52905; MUID:93339042; PMID:8339541
                                                                     collagen gene. Promoter
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A, Residues: 263-268 «MD».

A, Residues: 263-268 who.

A, Experimental source: skin

A, Note: attachment of 2-0-alpha-D-glucosyl-O-beta-D-galactose to 5-hydroxylysine

R, Labhard, M.E., Hollister, D.W.

Matrix 10, 124-130, 1990

A, Title: Segmental amplification of the entire helical and telopeptide regions of

A, Reference number: S15989; MUID:90326017; PMID:2374517
J. Biol. Chem. 260, 2315-2320, 1985
A;Title: Fine structural analysis of the human pro-alpha 1 (1)
A;Reference number: 155237; MUD:85130970; PMID:2857713
A;Accession: 155227
                                                                                                                                                                                                           A;Status: translation not shown; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-34 <CH2>
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A,Status: preliminary
A,Status: preliminary
A,Ratus: preliminary
A,Ratus: preliminary
A,Ratus: preliminary
A,Ratus: preliminary
A,Ratus: preliminary
A,Ratus: 1412-1433 - KET.

General: 112, 153 - KET.

M,Title: Nuclectide sequence of a cDNA clone for mouse proalphal(I) collagen protein.
A,Title: Nuclectide sequence of a cDNA clone for mouse proalphal(I) collagen protein.
A,Title: Nuclectide sequence of a cDNA clone for mouse proalphal(I) collagen protein.
A,Title: Nuclectide sequence of a cDNA clone for mouse proalphal(I) collagen protein.
A,Title: DANA construction and analysis.
A,Cross-deference 163-M142; NID:g19221; PIDN:AAA37333.1; PID:g19262
B,RACCESSION: LANA CONTROL ANALYSIS AND CONTROL ANALYSIS ANALY
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A; Title: The complete cDNA coding sequence for the mouse pro-alpha-1(I) chain of type A; Reference number: S57243
A; Rocession: S57243
A; Rocession: S57243
A; Residues: 1-1453 cliS>
A; Residues: 1-1453 cliS>
A; Residues: 1-1453 cliS>
A; Residues: D; de Crombrughe, B.; Vuorio, E. Biochim: Biophys. Acta 1089, 241-243, 1991
A; Accession: S57243
A; Accession: S57243
A; Reference number: S16176; MUID:91274355; PMID:2054384
A; Reference number: S16176; MUID:91274355; PMID:2054384
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   A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Molecules: 1187-1194, 'C',1196-1220 <COH>
A;Kossatues: 1187-1194, 'C',1196-1220 <COH>
A;Cross-references: GB:M23213; NID:g340842; PIDN:AABS9363.1; PID:g499622
A;Note: mutant sequence from a patient with mild osteogenesis imperfecta R;Maekelae, J.K.; Raassina, M.; Virta, A.; Vuorio, E.
Nucleic Acids Res. 16, 349, 1998
A;Title: Human pro-alpha-1(1) collagen: cDNA sequence for the C-propeptic
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95.6%; Pred. No. 5e-137;
live 21; Mismatches 3;
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Best Local Similarity 95.6
Matches 520; Conservative
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Collagen alpha 1(II) chain precursor [imported] - horse
NyAlternate names: type II collagen
NyAlternate names: type II collagen
CyBoteles: Squares caballus (domestic horse)
CyBoteles: 31-Jan-2000 #sequence_revision 31-Jan-2000 #text_change 04-Mar-2000
CyAccession: T45467
NyAlternate to the EMBL Data Library, June 1996
A;Bescription: Cloning of equine type II collagen and modulation of its expression in eq.
A;Reference number: 222977
A;Reference number: 222977
A;Residues: preliminary; translated from GB/EMBL/DDBJ
A;Residues: 1-1418 <RIC>
A;Residues: 1-1418 <RIC>
A;Coss-references: EMBL:U62528; PIDN:AAB05773.1
C;Superfamily: collagen alpha 1(1) chain; fibrillar collagen carboxyl-terminal homology;
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GPAGERGAPGSRGFPGADGIAGPKGPPGERGSPGAVGPKGSPGEAGRPGEAGLFGAKGLT
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A; Molecule type: protein
A; Molecule type: protein
A; Reperimental source: skin
A; Note: this is the latest in a series of papers from these workers elucidating the sequ
R; Byre, D.R; Glincher, M.J.
Biochem. Biochem. Biophys. Res. Commun. 48, 720-726, 1972
A; Title: Evidence for a previously undetected sequence at the carboxyterminus of the alp
A; Recession: A90181
A; Molecule type: protein
C; Commental source: skin
A; Note: residues 1037-1042 above correspond to the carboxyl end of the protein
C; Comment: Lypaines at positions 103, 700, 934, and 946 above may be hydroxylated in some
C; Comment: Pro-1002 is the prolines at the third position of the tripeptide repeating unit
C; Comment: Pro-1002 is the only 3-hydroxyproline and the only hydroxylated proline in pc
C; Superfamily: collagen alpha 1(1) relain; fibrillar collagen carboxyl-terminal homology;
C; Keywords: coiled coil; extracellular matrix, glycoprotein; pyroglutamic acid; trimer;
F; 1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
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C;Species: Gallus gallus (chicken)
C;Species: I2-Aug-1981 Hsequence_revision 06-Jul-1982 #text_change 31-Mar-2000
C;Accession: A90458; A90181; A02857
R;Highberger, J.H.; Corbett, C.; Dixit, S.N.; Yu, W.; Seyer, J.M.; Kang, A.H.; Gross, Blochemistry 21, 2048-2055, 1982
Biochemistry 21, 2048-2055, 1982
A;Tetle: Anino acid sequence of chick skin collagen alpha1(I)-CB8 and the complete priA;Reference number: A90458; MUID:82231995; PMID:7093229
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                                        GSPGSPGKTGPPGPAGQDGRPGPAGPPGPARGQAGVMGFPGPKGTAGEPGKAGERGLP
                                                                                                              GPPGAVGPAGKDGEAGAEGPPGPAGPAGERGEEGPAGSPGFEGLPGPAGPPGEAGKPGEE
                                                                                                                                     GVPGDLGAPGPSGARGEPGFPGERGVEGPPGPAGPPGADGAPGDDGAKGDAGAPGAPGSE
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A;Status: not compared with conceptual translation
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Molecule type: 2. 10.1' L', 83-103 <RYA2>
A;Note: alternative splice form 2; splicing appears to be under developmental regulation
R;Su, M.W.; Benson-Chanda, V.; Vissing, H.; Ramirez, F.
A;Title: Organization of the exons coding for Pro alpha-1(II) collagen N-propeptide conf
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A;Accession: S05000
A;Molecule type: DNA
A;Molecule type: DNA
A;Molecule type: DNA
A;Molecule type: DNA
A;Cross-deferences: EMBL:X16158; NID:929951; PIDN:CAA34278.1; PID:91335018; PIDN:CAA3427;
PIDN:CAA34283.1; PID:91335023; PIDN:CAA34284.1; PID:91335024
R;Rogaert, R.; Tiller, G.E.; Weis, M.A.; Gruber, H.E.; Rimoin, D.L.; Cohn, D.H.; Eyre, D.J. Boll. Chem. 267, 22522-22526, 1992
A;Title: An amino acid substitution (Gly853-->Glu) in the collagen alpha 1(II) chain proc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Molecule type: protein
A;Residues: 188-189, X', 191-195;1224-1230, 'X', 1232-1236 <DIA>
A;Residues: 188-189, X', 191-195;1224-1230, 'X', 1232-1236 <DIA>
B;Fanch, S.; Marzin, E.; Boutillon, M.M.; Lafont, R.; Lechene de la Porte, P.; Herbage, Eur. J. Biochem. 234, 125-131, 1995
A;Title: Immunohistochemical and biochemical analyses of 20000-25000-year-old fossil car A;Reference number: S63514; MUID:96096730; PMID:8529631
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         pri
                   A;Note: alternative splice form 1
R;Ryan, M.C.; Sandell, L.J.
A; Biol. Chem. 255, 10334-10339, 1990
A;Title: Differential expression of a cysteine-rich domain in the amino-terminal propept A;Reference number: A35428, MUID:90285153; PMID:2355003
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A, Residues: 171-172, C, 174-175 < ALA>

A, Residues: 171-172, C, 174-175 < ALA>

A, Note: mutant sequence from a family with family with primary generalized osteoarthriti

R, Diab, M, Wu, J.J.; Eyre, D.R.

Biochem. J. 314, 327-332, 1996

A, Title: Collagent type IX from human cartilage: a structural profile of intermolecular c

A, Reference number: $64673; MUID:96195147; PMID:8660302
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A, Molecule type: protein
A, Molecule type: protein
B, Molecule type: protein
A, R. Riller, G. B.; Weis, M.A.; Polumbo, P.A.; Gruber, H.B.; Rimoin, D.L.; Cohn, D.H.;
A, Tiller, G.B.; Weis, M.A.; Polumbo, P.A.; Gruber, H.B.; Rimoin, D.L.; Cohn, D.H.;
A, Tiller, G.B.; Weis, M.A.; Polumbo, P.A.; Gruber, H.B.; Rimoin, D.L.; Cohn, D.H.;
A, Tiller, An RNA-splicing mutation (G+51V320) in the type II collagen gene (COL2A1)
A, Reference number: 13867
A, Recession: 13867
A, Molecule type: DNA
A, Status: preliminary; translated from GB/EMBL/DDBJ
A, Molecule type: DNA
A, Residues: 440, G', 442-456, E', 458-480, 'P', 482-509 < TILL>
A, Cross-references: EMBL:U15195; NID:g557053; PIDN:AAB60370.1; PID:g557054
B; Ramirez, F
Submitted to the EMBL Data Library, December 1988
A, Reference number: S04892
A, Accession: S04892
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A, Status: nucleic acid seguence not shown; not compared with conceptual translation
A, Molecule type: DNA; mRNA
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A;Residues: 501-676, A',678-783,'A',785-831,'PA',834,'F',836-1214 <RAM>
A;Residues: 501-676, A',678-783, NID:930037; PIDN:CA932030.1; PID:9930050
R;Vikkula, M.; Peltonen, L.
R;Vikkula, M.; Peltonen, L.
R;Vikkula, M.; Peltonen, L.
A;Title: Structural analyses of the polymorphic area in type II collagen gasterence number: 805000; MUID:89325561; PMID:2753125
       PID:930041
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PIDN: CAA34683.1;
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A;Residues: 104-157, P', 159-236 cSUNA
A;Residues: 104-157, P', 159-236 cSUNA
A;Cross-treferences: GB:003065; GB:M23660; GB:M25655; GB:M2
A;Cross-treferences: GB:M23065; GB:M3
A;Cross-Natl. Acad. Sci. U.S.A. 87, 6565-6568, 1990
A;Title: Single base mutation in the type II procollagen g;Reference number: A94227; MUID:90370826; PMID:1975693
   A; Cross-references: EMBL:X16711; NID:g30040;
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                       GVPGDLGAPGPSGARGEPGFPGERGVEGPPGPAGPPGADGAPGDDGAKGDAGAPGAPGSE 360
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A;Cross-references: GB:M23759; NID:g180845; EMBL:X03320; GB:M24938; NID:g30104
A;Note: the GenBank PID is based on an incorrect reading frame
A;Accession: I37250
A;Status: translated from GB/EMBL/DDBJ
A;Nolecule type: DNA
A;Rolecule type: DNA
A;Rosicules: 541-560 <SAN3>
A;Rosicules: EMBL:X02378; GB:M23870; NID:g30107; PIDN:CAA26227.1; PID:g929621
A;Accession: I37251
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collagen alpha 1(II) chain precursor - mouse
C;Species: Mus musculus (house mouse)
C;Date: 28-May-1992 #sequence_revision 28-May-1992 #text_change 13-Aug-1999
C;Accession: A41182; A44885
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A;Title: Mouse type II collagen gene. Complete nucleotide seque: A;A;Ecerence number: A41182; MUID:91358489; PMID:1885613
A;Accession: A41182; MUID:91358489; PMID:1885613
A;Accession: preliminary; not compared with conceptual translation A;Molecule type: DNA....
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71.9%; Pred. No. 5e-100;
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A; Accession: A24561
A; Accession: A24561
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A; Accession: A24561
A; Mocecae to the code to the code
                             A; Residues: 752-831, 'PA', 834,'F', 836-1005,'K', 1007-1036,'O', 1038-1052,'E', 1054-1068,'T', A; Cross-references: GB:L00977; NID:g180812; PIDN:AAB23914.1; PID:g258774
A; Note: extracted from NCBI Dackbone (NCBIP:1173); parts of this sequence wer A; Note: this translation is not annotated and this publication is not cited in GenBank A; Note: mutant sequence associated with perinatal lethal hypochondrogenesis
A; Note: mutant sequence associated with perinatal lethal hypochondrogenesis
A; Tiller, G.B.; Rimoin, D.L.; Murray, L.W.; Cohn, D.H.
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A; Title: Tandem duplication within a type II collagen gene (COL2A1) exon in an individual and the control number: $16502; MUID:90251662; PMID:2339128
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A; Residues: 1245-1295 <STR1>
A; Cross-references: EMBL:X00339; EMBL:X00298; NID:g394699; PIDN:CAA25092.1; PID:g4378975
A; Accession: B21733
A; Molecule type: DNA
A; Molecule type: DNA
A; Residues: 894-909, 'PE' <STR2>
A; Cross-references: GB:K01785; NID:g30035; PIDN:CAA25082.1; PID:g1335032
A; Cross-references: GB:K01785; NID:g30035; M.F.; Martin, G.R.; Yamada, Y.
Biochemistry 24, 6343-6348, 1985
A; Title: Isolation and partial characterization of genomic clones coding for a human pro
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PMID:6320112
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A; Residues: 1164-1184, 'GPSGKDGANGIPGPI', 1185-1199 <TIL2>
A; Residues: 1164-1184, 'GPSGKDGANGIPGPI', 1185-1199 <TIL2>
A; Cross --references: EMBL:M37126; NID: 9180808; PIDN:AA52037.1; PID:9180809
A; Cross --references: EMBL:M37126; NID: 91809
A; Cheah, K.S.E.; Stoker, N.G.; Griffin, J.R.; Grosveld, F.G.; Solomon, E.
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A; Title: -Identification and characterization of the human type II collagen gene (COL2A1)
A; Reference number: A02858; MUID:85190534; PMID:3857598
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A; Residues: 1032-1056, NV, 1058-1068, T', 1070-1487 < CHE>
A; Residues: 1032-1056, NV, 1058-1068, T', 1070-1487 < CHE>
B; Elima, K.; Vuorio, T.; Vuorio, E.
Nuclaio, Caids Res. 15, 9499-9564, 1987
Nuclaio, Caids Res. 15, 9499-9564, 1987
A; Title: Determination of the single polyadenylation site of the human pro-alpha-1(II)
A; Reference number: A27280; MUID:88067771; PMID:2825137
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A, Molecule type: procein
A, Rolecule type: procein
A, Rolecule type: procein
A, Rolecule type: procein
A, Role: chondrocalcin identified as released collagen 1(II) chain carboxyl-terminal 1
R, Strom, C.M.; Upholt, W.B.
Nucleic Acids Res: 12, 1025-1038, 1984
A, Title: Isolation and characterization of genomic clones corresponding to the human
A, Reference number: A21733; MUID:84118798; PMID:6320112
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Arithe: Chondrocalcin is identical with the C-propeptide of type II procollagen.
A;Reference number: A57033; MUID:87099927; PMID:3800925
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A;Residues: 1175-1487 eELI>
A;Ccosa-references: EMBL:X06268; NID:G30096; PIDN:CAA29604.1; PID:G30097
A;Ccosa-reference: fetal epiphyseal cartilage
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A;Residues: 1-1419 <MET>
A;Cross-references: GB:M65161
R;Cheah, K.S; Lau, B.T.; Au, P.K.; Tam, P.P.
R;Cheah, K.S.; Lau, B.T.; Au, P.K.; Tam, P.P.
A;Cropment 111, 945-953, 1991
A;Title: Expression of the mouse alpha 1(II) collagen gene is not restricted to cartilage A;Reference number: A44885, MUID:91347939; PMID:1879363
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Query Match
Best Local Similarity 71.73
Matches 390; Conservative
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C,Species: Mus musculus (house mouse)
C,Gate: 28-May-1992 #sequence_revision 28-May-1992 #text_change 16-Jul-1999
C,Accession: B41182
C,Accession: B41182
C,Accession: Chem. 26, 1686-16869, 1991
A,Title: Mouse type II collagen gene. Complete nucleotide sequence, exon structure, and A,Racefactor: preliminary; not compared with conceptual translation
A,Molecule type: DNA
A,Residues: preliminary; not compared with conceptual translation
A,Residues: 1-1487 - MET.
A,Residues: 1-1487 - MET.
A,Residues: 1-1487 - MET.
A,Cross-references: GB:W65161
C;Superfamily: collagen alpha I(I) chain; fibrillar collagen carboxyl-terminal homology; C,Reywords: alternative splicing; coiled coil; extracellular matrix; glycoprotein; trime F;33-91/Domain: von Willabrand factor type C repeat homology <PRC>
F;1259-1487/Domain: fibrillar collagen carboxyl-terminal homology <PRC>
                 A; Molecule type: DNA
A; Molecule type: CNA
A; Residues: 1-28 cCHE.
A; Cross-references: GB: S63190; NID: g234368; PIDN: AAB19627.1; PID: g234369
A; Note: sequence extracted from NCBI backbone (NCBIN: 63190, NCBIP: 63192)
C; Superfamily: collagen alpha I(I) chain; fibrillar collagen extroxtyr-terminal homology; C; Keywords: alternative splicing; coiled coil; extracellular matrix; glycoprotein; trime F;1191-1419/Pomain: fibrillar collagen carboxyl-terminal homology <FCC>
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                                                                                                                                                         Query Match 71.3%; Score 2189; DB 2; Length 1419; Best Local Similarity 71.7%; Pred. No. 2.1e-99; Matches 390; Conservative 39; Mismatches 115; Indels 0
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A; Accession: A44885
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C;Species: Attus norvegicus (Norway rat)
C;Date: 13-Jul-1981 #sequence revision 13-Jul-1981 #text change 31-Mar-2000
C;Accession: A90559; A90552; A92029; A90353; A90566; A90357; A90362; A90379; A91209; A91
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A.A.Contents: CNBr0 and CNBr1
A.A.A.Contents: CNBr0 and CNBr1
A.A.R.Contents: A.B.Contein
A.R.Contents: A.B.Contein
A.R.Contents: 1-19 < 801-
A.R.Contents: 1-19 < 801-
A.R.Contents: A.B.Contein
A.R.Contents: A.B.Contein
A.R.Contents: A.B.Contein
A.R.Conteinental source: tendon
A.R.Conteinental sources from skin and tendon appear to be identical
A.Note: the amino-terminal tetrapeptide may be removed by limited proteolysis during a R.Kangy, A.H.; Bornstein, P.; Piez, K.A.
B.R.Conteinents: A.B.Contein, P.; Piez, K.A.
A.Title: The amino acid sequence of peptides from the cross-linking region of rat skin A.R.Contentor mumber: A90552; MUID: 67162268; PMID: 5337886
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                                                        Indels
                                                           115;
71.3%; Score 2189; DB 2; 71.7%; Pred. No. 2.1e-99; ive 39; Mismatches 115;
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A,Note: the composition of peptides comprising residues 1-9 and 1-19 confirms the sequence A,Note: this region (residues 651-671 above) probably corresponds to positions 1032-1052 (Comment: Prolines and lyaines at the third position of the tripeptide repeating unit (ed and subsequently 0-glycosylated.
C,Comment: The order of the nine CNBr peptides in the alpha 1(1) chain of rat skin collacy C,Comment: The complete chain contains 1052 residues.
C,Superfamily: collagen alpha 1(1) chain, fibrillar collagen carboxyl-terminal homology, C,Keywords: blocked amino end; coiled coil, serracellular matrix; glycoprotein, hydroxyl) F;1/Modified site: allysine (Lys) #status experimental
F;103,424,547/Binding site: carbohydrate (Lys) (covalent) #status experimental
F;103/Modified site: 5-hydroxylysine (Lys) (spartial) #status experimental
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collagen alpha 1(II) chain precursor - African clawed frog
6;Species: Aenopus laevis (African clawed frog)
6;Species: Aenopus laevis (African clawed frog)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C;Accession: B40333
R;Su, M.W.; Suzuki, H.R.; Bieker, J.J.; Solursh, M.; Ramirez, F.
J. Cell Biol. 115, 565-57, 1991
J. Cell Biol. 115, 555-57, 1991
J. Cell Biol. 115, 555-57, 1991
J. A/Title: Expression of two nonallelic type II procollagen genes during Xenopus laevis emt
A/Reference number: A40333; MUID:92011898; PMID:1918153
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A;Molecule type: mRNA
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Cross-references: 08:M65595
C;Superfamily: collagen alpha 1(I) chain; fibrillar collagen carboxyl-terminal homology;
C;Superfamily: collagen alpha 1(I) chain; fibrillar collagen carboxyl-terminal homology;
C;Keywords: colled coil; extracellular matrix; glycoprotein; triple helix
F;37-96/Domain: von Willebrand factor type C repeat homology <VWC>
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Matches 381; Conservative
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Ayacession: Agin Collagen Ayacession: Agin Collagen Ayacontens: Agin Collagen Ayacontens: Charles Structure of rat skin collagen alphal-CB8. Amino acid sequence of the hydroxyla Ayacontens: CMBr8
Ayacontens: 
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A.Residues: 419-567 <BU3>
Bur. J. Biochem. 37, 287-294, 1973
Bur. J. Biochem. 37, 287-294, 1973
A.Title: Structural and immunogenic properties of a major antigenic determinant in neutral A.Reference number: A91209; MUID:74011954; PMID:4126850
A.Rocession: A91209
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                                                                                                                                                      Afacession: A92029
A/Molecule type: protein
A/Experimental source: skin and tendon
B/Buchemistry 10, 2076-2081, 1971
A/Fitle: Chemical studies on the cyanogen bromide peptides of rat skin collagen. Amino
A/Reference number: A90353; MUID:71263178; PMID:4327399
A/Accession: A90353
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A/Residues: 239-418 <BA2>
A/Residues: 239-418 <BA2>
A/Residues: 239-418 <BA2>
B/Experimental source: skin.
R/Butler, W.T.; Underwood, S.P.; Finch Jr., J.E.
Biochemistry 13, 2946-2953, 1974
A/Title: Chemical studies on the cyanogen bromide peptides of rat skin collagen. Amino A/Recence number: A90379; MUID:74271984; PMID:4366532
A/Accession: A90379
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A/Residues: 568-61 csrlv.
A/Residues: 568-61 csrlv.
A/Note: this region probably corresponds to positions 949-1032 of the alpha 1(I) chain
A/Note: the major antiquence determinant (of neutral salt-extracted rat skin collagen)
A/Note: the major antiquence determinant (of neutral salt-extracted rat skin collagen)
B/Stoltz, M.; Timpl, R.; Kuehn, K.
FEBS Lett. 26, 61-65, 1972
A/Title: Non-helical regions in rat collagen alphal-chain.
A/Reference number: A91385; MUD:73049495; PMID:4636751
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          skin collagen. The
J. Biol. Chem. 242, 2572-2574, 1967
A/Title: The incomplete hydroxylation of individual prolyl residues in collagen.
A/Reference number: A92029; MUID:67165368; PMID:4290711
A/Contents: CNBr2
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R, Butler, W.T.
Biochemistry 9, 44-50, 1970
A, Title: Chemical studies on the cyanogen bromide peptides
A, Reference number: A90566; MUID:70085124; PMID:5411206
A, Contents: CNBr5
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Residues: 56-102 <BUI>
Experimental source: skin
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A;Molecule type: protein
A;Essidues: 651-671 <ST2>
A;Experimental source: skin
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A; Molecule type: protein
A;Residues: 20-145 <FIE>
A;Residues: 20-145 <FIE>
A;Residues: 20-145 <FIE>
A;Residues: 20-145 <FIE>
A;Ryperimental source: skin
A;Vote: Lys-103 is Mydroxylated and binds glucosylgalactose
A;Vote: Lys-103 is Mydroxylated and binds glucosylgalactose
R;Fietzek, P.P.; Wendt, P.; Kell, I.; Kuehn, K.
FEBS Lett. 26, 74-76, 1972
FA;Title: The covalent structure of collagen: amino acid sequence of alphal-CB3 from calf
A;Reference number: A91387; MUID:73049499; PMID:4673951
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C;Species: Bos primigenius taurus (cattle)
C;Species: 24-Apr-1964 Hacquence revision 31-Dec-1993 #text_change 31-Mar-2000
C;Accession: A91193; A91229; A91387; A91211; A91201; A91200; A43048; A02853
R;Rauterberg, J.; Timpl, R.; Furthmayr, H.
Eur. J. Blochem. 27, 231-237, 1972
A;Title: Structural characterization of N-terminal antigenic determinants in A;Reference number: A91193; MuID:72255334; PMID:4115172
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                            GPGGPPGPKGDSGEPGAPGSKGDTGAKGEPGPVGVEGPPGPAGEEGKPGARGEPGPTGLP
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A, Residues: 1-19 <RAU>
A, Residues: 1-19 <RAU>
A, Experimental source: skin
A, Note: the epsilon carbon of Lys-9, by homology with the rat alpla; Fietzek, P.P.; Kuehn, K.
B.W. J. Biochem. 52, 77-82, 1975
A, Title: The covalent structure of collagen: amino-acid sequence A, Reference number: Ap1229; MUID: 76022320; PMID: 1164916
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A, Residues: 146-294 <FI2>
A, Experimental source: skin
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C;Species: Xenopus laevis (African clawed frog)
C;Date: 16-Sep-192 #sequence_revision 16-Sep-1992 #text_change 16-Jul-1999
C;Accession: A40333
R;Su, M.W.; Suzuki, H.R.; Bieker, J.J.; Solursh, M.; Ramirez, F.
J. Cell Biol. 115, 565-575, 1991
A;Title: Expression of two nonallelic type II procollagen genes during Xenopus laevis em A;Reference number: A40333; MUID:920118989; PMID:1918153
A;Accession: A4033
A;Accession: A4033
A;Reference number: A40333
A;Reference number: A60335
A;Reference number: A60335
A;Residues: 11492 <SUA>
A;Cross-references: GB:M63596
A;Note: this sequence is presented as substitutions relative to another sequence in a fide they replace; the appropriate interpretation of the sequence figure was reconstructed C;Superfamily: collagen alpha 1(I) chain; fibrillar collagen carboxyl-terminal homology; C;Keywords: coiled coil; extracellular matrix; glycoprotein; trimer; triple helix F;7-96/Domain: von Willebrand factor type C repeat homology <VWC>
F;1263-1492/Domain: the fibrillar collagen carboxyl-terminal homology <
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69.4%; Score 2131; DB 2;
Best Local Similarity 70.0%; Pred. No. 1.4e-96;
Matches 381; Conservative 41; Mismatches 122;
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41; Mismatches 120;
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collagen alpha 2(V) chain precursor - human
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Bur. 'D. Biochem. 30, 169-183, 1972

A'Reference number: A91201, MUID:7304276; PMID:4343808

A'Reference number: A91201, MUID:7304276; PMID:4343808

A'Reference number: A91201, MUID:7304276; PMID:4343808

A'Residues: 563-675 <WEN>
A'Reference number: A91200, MUID:73042275; PMID:4343807

A'Reference number: A91200, MUID:73042275; PMID:4343807

A'Rocession: A91200

A'Molecule type: protein
A'Reference number: A91200, MUID:73042275; PMID:4343807

A'Roter Pro-726 is the only 3-hydroxyproline and the only hydroxylated proline in positi
B'Raperimental source: skin
A'Note: Pro-726 is the only 3-hydroxyproline and the only hydroxylated proline in positi
FEBS Lett. 21, 75-79, 1972

A'Itle: The amino acid sequence of the carbòxyterminal nonhelical cross link region of
A'Rocession: A43048
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A/Accession: A43048
A/Molecule type: protein
A/Experimental source: skin
C/Comment: Dysines at positions 115, 124, 274, 346, 424, 496, 658, and 670 may be hydrox
C/Comment: Prolines in the third position of the tripeptide repeating unit (G-X-Y) are h
C/Comment: The order of the eight CNBr peptides in the alpha 1(1) chain of bovine skin of
C/Comment: The complete chain contains 1052 residues.
C/Superfamily: collagen alpha 1(1) chain; fibrillar collagen carboxyl-terminal homology;
C/Superfamily: collagen alpha 1(1) chain; fibrillar collagen carboxyl-terminal homology;
C/Keywords: coiled coil; extracellular matrix; glycoprotein; pyroglutamic acid; trimer;
F/1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
R;Fietzek, P.P.; Rexrodt, F.W.; Hopper, K.E.; Kuehn, K.
Eur. J. Blochem. 38, 386-400, 1973
A;Title: The covalent structure of collagen. 2. The amino-acid sequence of alphal-CB7 fr
A;Reference number: A91211; MUID:74086118; PMID:4359390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         234
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   341 GAPGDKGEAGPSGPA---GTRGAPGDRGEPGPPGPAGFAGPPGADGOPGAKGEPGDAGAK 397
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   175 GAKGLTGSPGSPGPDGKTGPPGPAGEDGRPGPPGPPGARGEAGVMGFPGPKGAAGEPGKA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  295 GKPGEEGVPGDLGAPGPSGARGEPGFPGERGVEGPPGPAGPPGADGAPGDDGAKGDAGAP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 67.6%; Score 2076.5; DB 1; Length 779; Best Local Similarity 78.0%; Pred. No. 3.7e-94; Matches 382; Conservative 18; Mismatches 51; Indels 39;
                                                                                                                A;Accession: A91211
A;Molecule type: protein
A;Residues: 295-562 <FI3>
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A. Experimental source: placenta

Rigreenspan, D.S.; Lee, S.T.; Lee, B.S.; Hoffman, G.G.
Gene Expr. 1, 29-39, 1991

A; Experimental source: placenta

Rigreenspan, D.S.; Lee, S.T.; Lee, B.S.; Hoffman, G.G.
Gene Expr. 1, 29-39, 1991

A; Experimental source: placenta

A; Reference number: A54555; MUD: 92314691; PMID: 1820205

A; Accession: A54555

A; Accession: A54555

A; Molecule type: DNA

A; Residues: 1-32 <GRE>
A; Molecule type: DNA

A; Residues: 1-32 <GRE>
A; Moradi-Ameli, M.; Rousseau, J.C.; Kleman, J.P.; Champliaud, M.F.; Boutillon, M.M.; Berr

Eur. J. Biochem: 221, 987-995, 1994

A; Title: Diversity in the processing events at the N-terminus of type-V collagen.
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A, Cross-references: GB-M10956, NID:g180427; FIDN:AAA52007.1; FID:g180428
A; Cross-references: GB-M10956, NID:g180427; FIDN:AAA52007.1; FID:g180428
A; Note: part of this sequence were GB-FERMING Sequencing
R; Emanuel, B.S.; Cannizzaro, L.A.; Seyer, J.M.; Myers, J.C.
R; Emanuel, B.S.; Cannizzaro, L.A.; Seyer, J.M.; Myers, J.C.
A; Emanuel, B.S.; Cannizzaro, L.A.; Seyer, J.W.; Myers, J.C.
A; The Common Sequence of the Sequence of the long arm A; Reference number: IS9025; MID:38216505; MMID:3858826
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C;Species: Homo sapiens (mai)
C;Date: 31-Jul-1989 #sequence revision 28-Jul-1995 #text_change 31-Dec-2000
C;Date: 31-Jul-1989 #sequence revision 28-Jul-1995 #text_change 31-Dec-2000
C;Date: 31-Jul-1989 #sequence revision 28-Jul-1995 #text_change 31-Dec-2000
R;Woodbury, D.; Benson-Chanda, V.; Ramirez, F.
J. Biol. Chem. 264, 2735-2738, 1989
A;Title: Amino-terminal propeptide of human pro-alpha2(V) collagen conforms to the A;Reference number: A31427, MUID:89123368; PMID:2914927
534
                                              398 GDAGPPGPAGPAGPPGPPGPIGNVGAPGPKGARGSAGPPGATGFPGAAGRVGPPGPGPSGNAGPP 457
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A;Residues: 1-463 <WOO>
A;Cross.references: GB:J04478; NID:g179697; PIDN:AAA51859.1; PID:g179698
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A,Residues: 338-1496 *MEI>
A,Residues: 338-1496 *MEI>
A,Cross-references: GBXX04758; NID:g29588; PIDN:CAA28454.1; PID:g1340175
A;Experimental source: rhabdomyosarcoma cell line
R;Myers, J.C.; Loidl, H.R.; Stolle, C.A.; Seyer, J.M.
J. Bioll Chem. 260, 5533-5541, 1895
A;Title: Partial covalent structure of the human alpha 2 type V collagen
A;Reference number: 155239; MUID:85182703; PMID:2985598
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A,Molecule type: protein
A,Residues: 288-291, 'P',293-294,'X',295-297;606,'X',608-617 <MOR>
R,Weil, D.; Bernard, M.; Gargano, S.; Ramirez, F.
R,Weil, D.; Bernard, M.; Gargano, S.; Ramirez, F.
M.Worleic Adda Res. 15, 181-198, 1987
A,Title: The pro alpha 2 (V) collagen gene is evolutionarily relative. A,Reference number: A25874; MUID:87146331; PMID:3029669
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      pro alpha 2(I) collagen
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C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Dacession: A42291, A54328
R;Phillips, C:L; Morgan, A.L.; Lever, L.W.; Wenstrup, R.J.
Genomics 13, 1345-1346, 1992
A;Title: Sequence analysis of a full-length cDNA for the murine pro alpha 2 A;Reference number: A43291; MUID:92372043; PMID:1505972
A;Reference number: A43291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Status: preliminary; not compared with conceptual translation
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Cross-references: GENSB251; NID:g50488; PIDN:CAA41205.1; PID:g50489
A;Cross-reference extracted from NCBI backbone (NCBIP:112027)
B;Phillips, C.L.; Lever, L.W.; Pinnell, S.R.; Quarles, L.D.; Wenstrup, R.J.
A;Title: Construction of a full-length murine Proalpha2(I) collagen cDNA by
                                                                                                                                                                                                                                                                GPPGAVGPAGKDGEAGAEGPPGPAGPAGERGEEGPAGSPGFEGLPGPAGPPGEAGKPGEE
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                                     813 GEPGPRGLVGPPGSRGNPGSRGENGPTGAVGFAGPQGSDGQPGVKGEPGEPGAGDAGSP
   121 GPPGERGGPGSRGFPGADGVAGPKGPAGERGSPGPAGPKGSPGEAGRPGEAGLPGAKGLT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GESGPSGPAGPTGARGAPGDRGEPGPPGPAGFAGPPGADGEPGAKGEPGDAGAKGDAGPP
                                                                                                                     GSPGSPGPDGKTGPPGPAGEDGRPGPPGPPGARGEAGVMGFPGPKGAAGEPGKAGERGVP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GAPGLEGMPGERGAAGLPGPKGDRGDAGPKGADGSPGKDGVRGLTGPIGPPGPAGAPGDK
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64.2%; Pred. No. 3.7e-86;
iive 45; Mismatches 150;
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A;Residues: 1-110 <PH2>
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                                                                                                                                                                                                                                          241
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C. Gomment: The amino-terminal propeptide domain appears not to be completely cleaved. C. Gomment: The amino-terminal propeptide domain appears not to be completely cleaved.

A. Genes (GBB:CGSA2

A. Genes (GBB:CGSA2

A. Map position: 261-261

F. J. S. Map position: 261-261

F. J. S. Map position: 261-261

F. J. J. S. Map position: 261-261

F. J. J. J. J. Map position: 261-261

F. J. J. J. Map positio
A;Accession: A25374
A;Molecule type: mRNA
A;Residues: 122-1417, Tr. 1419-1437, Sr.,1439-1496 cMYE>
A;Molecule type: mRNA
A;Residues: 122-1417, Tr. 1419-1437, Sr.,1439-1496 cMYE>
A;Cross-references: GB:M11718; NID:g180912; PIDN:AA52058.1; PID:g180913
A;Experimental source: normal fibroblasts
R;Tsipouras, P.; Schwartz, R.C.; Liddell, A.C.; Salkeld, C.S.; Weil, D.; Ramirez, F. Genomics 3, 275-277, 1988
A;Title: Genetic distance of two fibrillar collagen loci, COL3A1 and COL5A2, located on A;Reference number: A30017, MUD:89138450; PMID:3224983
A;Accession: A30017
A;Accession: A30017
A;Residues: 1449-1463, Er.,1465-1495, A. <4TSI>
A;Cross-references: GB:J03051; NID:g179695; PIDN:AA51858 1; PID:g179696
A;Cross-references: GB:J03051; NID:g179695; PIDN:AA51858 1; PID:g179696
C;Comment: Drolines and lysines at the third position of the tripeptide repeating unit (are 5-hydroxylated and subsequently O-glycosylated.
C;Comment: The amino-terminal propeptide domain appears not to be completely cleaved.
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Best Local Similarity 64.0%;
Matches 348; Conservative 4
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A;Cross-references: EMBL:X57983; NID:gS0476; PIDN:CAA41048.1; PID:g50477
GGenteics:
A;Introns: 29/1; 95/3; 112/3; 150/3; 175/3; 193/3; 211/3; 229/3; 247/3; 265/3; 283/3; 296
58/3; 673/3; 706/3; 742/3; 760/3; 778/3; 796/3; 860/3; 868/3; 886/3; 886/3; 800/3; 976/3; 750/9; 750/9; 710/9; 710/9; 710/9; 710/9; 710/9; 710/9; 710/9; 710/9; 710/9; 710/9; 710/9; 710/9; 710/9; 710/9; 710/9; 710/9; 710/9; 710/9; 710/9; 710/9; 710/9; 710/9; 710/9; 710/9; 710/9; 710/9; 710/9; 710/9; 710/9; 710/9; 710/9; 710/9; 710/9; 710/9; 710/9; 710/9; 710/9; 710/9; 710/9; 710/9; 710/9; 710/9; 710/9; 710/9; 710/9; 710/9; 710/9; 710/9; 710/9; 710/9; 710/9; 710/9; 710/9; 710/9; 710/9; 710/9; 710/9; 710/9; 710/9; 710/9; 710/9; 710/9; 710/9; 710/9; 710/9; 710/9; 710/9; 710/9; 710/9; 710/9; 710/9; 710/9; 710/9; 710/9; 710/9; 710/9; 710/9; 710/9; 710/9; 710/9; 710/9; 710/9; 710/9; 710/9; 710/9; 710/9; 710/9; 710/9; 710/9; 710/9; 710/9; 710/9; 710/9; 710/9; 710/9; 710/9; 710/9; 710/9; 710/9; 710/9; 710/9; 710/9; 710/9; 710/9; 710/9; 710/9; 710/9; 710/9; 710/9; 710/9; 710/9; 710/9; 710/9; 710/9; 710/9; 710/9; 710/9; 710/9; 710/9; 710/9; 710/9; 710/9; 710/9; 710/9; 710/9; 710/9; 710/9; 710/9; 710/9; 710/9; 710/9; 710/9; 710/9; 710/9; 710/9; 710/9; 710/9; 710/9; 710/9; 710/9; 710/9; 710/9; 710/9; 710/9; 710/9; 710/9; 710/9; 710/9; 710/9; 710/9; 710/9; 710/9; 710/9; 710/9; 710/9; 710/9; 710/9; 710/9; 710/9; 710/9; 710/9; 710/9; 710/9; 710/9; 710/9; 710/9; 710/9; 710/9; 710/9; 710/9; 710/9; 710/9; 710/9; 710/9; 710/9; 710/9; 710/9; 710/9; 710/9; 710/9; 710/9; 710/9; 710/9; 710/9; 710/9; 710/9; 710/9; 710/9; 710/9; 710/9; 710/9; 710/9; 710/9; 710/9; 710/9; 710/9; 710/9; 710/9; 710/9; 710/9; 710/9; 710/9; 710/9; 710/9; 710/9; 710/9; 710/9; 710/9; 710/9; 710/9; 710/9; 710/9; 710/9; 710/9; 710/9; 710/9; 710/9; 710/9; 710/9; 710/9; 710/9; 710/9; 710/9; 710/9; 710/9; 710/9; 710/9; 710/9; 710/9; 710/9; 710/9; 710/9; 710/9; 710/9; 710/9; 710/9; 710/9; 710/9; 710/9; 710/9; 710/9; 710/9; 710/9; 710/9; 710/9; 710/9; 710/9; 710/9; 710/9; 710/9; 710/9; 710/9; 710/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               collagen alpha 1(III) chain precursor - mouse C; Species: Mus musculus (house mouse) C; Species: Mus musculus (house mouse) C; Date: 10-Apr-1996 #sequence revision 19-Apr-1996 #text_change 13-Aug-1999 C; Accession: S59865, S62120; $16373 R; Toman, P.D.; de Crombrugdhe, B. Gene 147, 161-166, 1994 A; Title: The mouse type-III procollagen-encoding gene: genomic cloning and complete DNA, A; Reference number: S59856; MUID:95011609; PMID:7926795
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                                        574 GNPGVOGPEGKLGPLGAPGEDGRPGPPGSIGIRGOPGSMGVPGPKGSSGDLGKPGEAGNA
                                                                                                                                                                                                                                                         GVPGDLGAPGPSGARGEPGFPGERGVEGPPGPAGPPGADGAPGDDGAKGDAGAPGSE
                                                                                                                                                                                  634 GVPGQRGAPGKDGEVGPSGPVGPPGLAGERGEAGPPGPTGFQGLPGPPGPPGEGGKAGDQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                          754 GPPGLQCMPGERGIAGTPGPKGDRGGIGEKGAEGTAGNDGARGLPGPLGPPGPAGLLGAP
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                                                                                                               GPPGAVGPAGKDGEAGAEGPPGPAGPAGERGEEGPAGSPGFEGLPGPAGPPGEAGKPGEE
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A;Reference number: $62120

A;Accession. $65120

A;Accession. $65120

A;Accession. $65120

A;Residues: 1-866,'G', 868-1464 <TOA>
A;Residues: 1-866,'G', 868-1464 <TOA>
A;Cross-references: EMBL:X52046; NID:g575321; PIDN:CAA36279.1; PID:g575322

A;Accession. Biophys. Acta 1089, 241-343, 1991

A;Title: Specific hybridization probes for mouse type I, II, III and IX coll
A;Reference number: $16176; MUD:91274355; PMID:2054384

A;Accession: $16373

A;Accession: $16373

A;Return argument 
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,32-92/Domain: von Willebrand factor type C repeat homology <VWC>
155-1464/Product: collagen alpha 1(III) chain #status predicted <MAT>
;1236-1464/Domain: fibrillar collagen carboxyl-terminal homology <FCC>
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Similarity 63.3%; Pred. No. 8.5e-86;
16; Conservative 37; Mismatches 158;
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A;Residues: 1-1464 <TOM>
A;Cross-references: EMBL:X52046
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C;Species: Mus musculus (house mouse)
C;Date: 02-Jul-1996 #text_change 13-Aug-1999
C;Accession: 149607
R;Andrikopoulos, K.; Suzuki, H.R.; Solursh, M.; Ramirez, F.
Dev. Dyn. 195, 113-120, 1992
A;Title: Localization of pro-alpha 2(V) collagen transcripts in the tissues of t A;Reference number: 149607; WUID:93214071; PMID:1297453
A;Accession: 149607
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-1497 <RES>
A;Cross-references: GB:LO2918; NID:g309180; PIDN:AAA37440.1; PID:g309181
C;Genetics:
A;Gene: Colsa-2
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US-10-658-989A-4 3070 1 GSBGPEGVRGEPGPPGPAGA.....PGPSGDAGPRGPPGPAGKEG 544 Title: Perfect score: 3 Sequence:

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SEQUENCE OF 1-44 FROM N.A.
MEDLINE-88033098; PubMed-2822714;
Rossouw C.M.S., Vergeer W.P., du Plooy S.J., Bernard M.P., Ramirez F.,
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"RNA sequence analysis of a perinatal lethal osteogenesis imperfecta
mutation..;
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MEDIATE=89109573; PubMed=2913053;
CODSTANTINE=89109573; Prockop D.J.;
"A lethal variant of osteogenesis imperfecta has a single base mutaction that substitutes cysteine for glycine 904 of the alpha 1(I) entation that substitutes cysteine for glycine 904 of the alpha 1(I) chain of type I procollagen. The asymptomatic mother has an unidentified mutation producing an overmodified and unstable type I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WARIANT OI CYS-1195.
MEDLINE-89218628; PubMed=2244312;
Labhard M.E., Witz-Z M.K., Pope F.M., Nicholls A.C., Hollister D.W.;
"A cysteine for glydine substitution at position 1017 in an alpha
1(1) chain of type I collagen in a patient with mild dominantly
inherited osteogenesis imperfecta.";
MEDLINE-88033031; PubMed-3667599;
Vogel B.E., Minor R.R., Freund M., Prockop D.J.;
"A point mutation in a type I procollagen gene converts glycine 748
the alpha I chain to cysteine and destabilizes the triple helix:
a lethal variant of costeogenesis imperfecta.";
J. Biol. Chem. 262:14737-14744(1987).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VARIANTS OI-II ALA-1106, VAL-1151; ARG-1154 AND VAL-1184.
MEDLINE-89380165; PubMed-2777764;
Lamande S.R., Dahl H.-H.M., COLe W.G., Bateman J.F.;
"Characterization of point mutations in the collagen COLIA1 and COLIA2 genes causing lethal perinatal osteogenesis imperfecta.";
J. Biol. Chem. 264:15809-15812(1989).
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VARIANT OI-II ARG-842.
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   Length 1464;
                               3; Indels
96.6%; Score 2966; DB 1; 95.6%; Pred. No. 2.5e-113; ive 21; Mismatches 3;
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DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 15-MAR-2004 (Rel. 39, Last sequence update)
DT 15-MAR-2004 (Rel. 39, Last sequence update)
DT 15-MAR-2004 (Rel. 39, Last sequence update)
DE Collagen alpha 1(1) chain precursor.
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OX NCBL TaxID=9615;
RN | [1]
RR SEQUENCE FROM N.A., AND VARIANT OI ALA-208.
RX MEDLINE=21023337; PubMed=11147834;
RX MEDLINE=21023337; PubMed=11147834;
RX MEDLINE=21023337; PubMed=11147834;
RX Campbell B.G., Wootton J.A.M., MacLeod J.N., Minor R.R.;
RY "Sequence of normal canine COLIA1 CDNA and identification of a RT "Sequence of normal canine COLIA1 CDNA and identification of a RT canine osteogenesis imperfecta.";
RY of canine osteogenesis imperfecta.";
RY ACBURTON: Type I collagen is a member of group I collagen CC -1- FUNCTION: Type I collagen is a member of group I collagen CC -1- FUNCTION: Type I collagen is a member of group I collagen CC -1- FUNCTION: Type I collagen is a member of group I collagen CC -1- FUNCTION: Type I collagen is a member of group I collagen CC -1- FUNCTION: Type I collagen is a member of group I collagen CC -1- FUNCTION: Type I collagen is a member of group I collagen CC -1- FUNCTION: Type I collagen is a member of group I collagen CC -1- FUNCTION: Type I collagen is a member of group I collagen is a member of
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8 8 8

597 657 717 GAPGLEGMPGERGAAGLPGPKGDRGDAGPKGADGSPGKDGVRGLTGPIGPPGPAGAPGDK 420 241 GPPGAVGPAGKDGEAGAEGPPGPAGPAGERGEEGPAGSPGFEGLPGPAGPPGEAGKPGEE 300 GVPGDLGAPGPSGARGEPGFPGERGVEGPPGPAGPPGADGAPGDDGAKGDAGAPGAPGSE 360 538 GSPGSPGPDGXTGPPGPAGDGRPGPPGPPGARGQAGVWGFPGPKGAAGEPGKAGERGVP 301 658 361 Dp δ ò g à d $\stackrel{>}{\circ}$

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NONHELICAL REGION (C-TERMINAL).

N-LINKED (GLCNAC. .) (POTENTIAL).

CELL ATTACHMENT SITE (POTENTIAL).

CELL ATTACHMENT SITE (POTENTIAL).

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COLLAGEN ALPHA 1 (I) CHAIN.
CARBOXYL-TERMINAL PROPEPTIDE.
VWFC.
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EMBL; K03032; AAA37332.1; JOINED.
EMBL; K03033; AAA37332.1; JOINED.
EMBL; K03034; AAA37332.1; JOINED.
EMBL; K03035; AAA37332.1; JOINED.
PIR; S57243; S21226.
MGD; MGI:88467; COlla1.
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InterPro; IPRO08166; Collagen.
InterPro; IPRO00865; Fib collagen.
InterPro; IPRO02181; Fibrinogen_C.
                                                                                                                                                                                                                                                                                                    EMBL, M14423, AAA37333.1, -.
EMBL; M17491, AAA37334.1; -.
EMBL; X06753; CAA29927.1; -.
EMBL; K03036, AAA37332.1; -.
EMBL; K03029; AAA37332.1; JOINED.
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P SEQUENCE OF 1442-1453 FROM N.A.

MEDLINE=88124276; PubMed=3140560;

MA MOOSLehner K., Harbers K.;

R Two mRNAs of mouse pro alpha 1(I) collagen gene differ in the size of the 3 'untranslated region.";

R Of the 3 'untranslated region.";

R Nucleic Acids Res. 16:773-773(1988).

CC -: FUNCTION: Type I collagen is a member of group I collagen

CC -: FUNCTION: Type I collagen).

CC -: SUBUNT: Trimers of one alpha 2(I) and two alpha 1(I) chains.

CC -: SUBUNT: Trimers of one alpha 2(I) and two alpha 1(I) chains.

CC -: TISSUE SPECIFICITY: Forms the fibrils of tendon, ligaments and bones. In bones the fibrils are mineralized with calcium

L.A.C.V.MANARITE.
                                                                                                                                                                                         838 GPAGPTGPPGPIGNVGAPGPKGARGSAGPPGATGFPGAAGRVGPPGPSGNAGPPGPPGPA
                                     GESGPSGPAGPTGARGAPGDRGEPGPPGPAGFAGPPGADGEPGAKGEPGDAGAKGDAGPP
                                                                        MEDLINE=9603340; PubMed=8535610;
Li S.W., Khillan J., Prockop D.J.;
"The complete cDNA coding sequence for the mouse pro alpha 1(1) chain
                                                                                                                                                       GPAGPAGPPGPIGDVGAPGAKGARGSAGPPGATGFPGAAGRVGPPGPSGDAGPPGPPGPA
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MEDLINE=83141374; PubMed=6298597;
Monson J.M., Friedman J., McCarthy B.J.;
"DNA sequence analysis of a mouse pro alpha 1 (I) procollagen gene:
evidence for a mouse B1 element within the gene.";
Mol. Cell. Biol. 2:1362-1371(1982).
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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French B.T., Lee W.-H., Maul G.G.;
"Nucleotide sequence of a cDNA clone for mouse pro alpha 1(I)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CA11 MOUSE STANDARD; PRT; 1453 AA. P1087, Q60635; Caeated) 01-UUL-1989 (Rel. 11, Created) 01-NOV-1997 (Rel. 35, Last sequence update) 28-FEB-2003 (Rel. 41, Last annotation update) collagen alba 1(I) chain precursor.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   of type I procollagen.";
Matrix Biol. 14:593-595(1995).
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SEQUENCE OF 518-1128 FROM N.A.
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Gene 39:311-312(1985).
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830 GPAGPAGPPGPIGDVGAPGAKGARGSAGPPGATGFPGAAGRVGPPGPSGDAGPPGPPGPA 540 GESGPSGPAGPTGARGAPGDRGEPGPPGPAGPAGPPGADGEPGAKGEPGDAGAKGDAGPP 480 GPPGAVGPAGKDGEAGAEGPPGPAGPAGERGEEGPAGSPGFEGLPGPAGPPGEAGKPGEE 300 GPPGAVGPAGKDGEAGAQGAPGPAGPAGPAGERGEQGPAGSPGFQGLPGPAGPPGBAGKPCBQ 650 GVPGDLGAPGPSGARGEPGFPGERGVEGPPGPPGADGAPGDDGAKGDAGAPGAPGSE 360 GAPGLEGMPGERGAAGLPGPKGDRGDAGPKGADGSPGKDGVRGLTGPIGPPGPAGAPGDK 420 Gallus gallus (Chicken). Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae; end the carboxyterminus MEDINE-8231995, PubMed=7093229, Highberger J.M., Corbett C., Dixit S.N., Yu W., Seyer J.M., Kang A.H., Gross J.; Annino acid sequence of chick skin collagen alpha 1(I)-CBB and the complete primary structure of the helical portion of the chick skin collagen alpha 1(I) chain."; SECUENCE OF 1-153 FROM N.A.
MEDLINE-88056316; PubMed=3678834;
Finer M.H., Boedtker H., Doty P.;
Foner M.H., Boedtker H., Doty P.;
Construction and characterization of cDNA clones encoding the 5'
of the chicken pro alpha 1(I) collagen mRNA."; SEQUENCE OF 1-144 FROM N.A.

MEDLINE=88007542; PubMed=2820966;
Finer M.H., Aho S., Gerstenfeld L.C., Boedtker H., Doty P.;
Finer M.H., Aho S., Gerstenfeld L.C., Boedtker Fr., Doty P.;
"Unusual DNA sequences located within the promoter region and the first intron of the chicken pro-alpha 1(1) collagen gene.";
J. Biol. Chem. 262:13323-13332(1987). SEQUENCE OF 1200-1205.
MEDLINE=72243016; PubMed=5047697;
Eyre D.R., Glimcher M.J.;
Eridence for a previously undetected sequence at of the alpha 1 chain of chicken bone collagen.";
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its modified anothris institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
"Sequence determination and analysis of the 3' region of chicken proalpha 1(I) and pro-alpha 2(I) collagen messenger ribonucleic acids including the carboxy-terminal propeptide sequences.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DR PIR; A27179; A27179
                                                                                                                          MEDLINE=80134546; PubMed=6987088;
MEDLINE=80134546; PubMed=6987088;
Panoaller A.M., Pesciotta D.M., Eikenberry E.F., Yamamoto T.,
Panoaller A.M., Pesciotta D.M., Eikenberry E.F., Yamamoto T.,
Pastan I., Decrembrughe B., Fietzek P.P., Olsen B.R.;
"Nucleotide sequence of a collagen cDNA-fragment coding for the carboxyl end of pro alpha 1(1)-chains.";
FEBS Lett. 11:61-65(1980).
-!- FUNCTION: Type I collagen is a member of group I collagen
(fibrillar forming collagen).
-!- SUBMIT: Trimers of one alpha 2(I) and two alpha 1(I) chains.
-!- TISSUE SPECIFICITY: Forms the fibrils of tendon, ligaments and bones. In bones the fibrils are mineralized with calcium
                                                                                                                                                                                                                                                                                                                                                                                                                              hydroxyapatite.
-!- PTM: Proline residues at the third position of the tripeptide repeating unit (G-X-Y) are hydroxylated in some or all of the chains. Pro-1153 is the only 3-hydroxypro and the only hydroxylated proline in position X.
-!- SIMILARITY: Contains 1 VWFC domain.
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PYRROLIDONE CARBOXYLIC ACID.

HYDROXYLATION (POTENTIAL).

HYDROXYLATION (POTENTIAL).

HYDROXYLATION (POTENTIAL).

HYDROXYLATION (POTENTIAL).

HYDROXYLATION.

F -> L (IN REF. 5).

Q -> H (IN REF. 6).

WW; 3EC6152134271F4D CRC64;
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89.0%; Pred. No. 1.2e-105;
iive 28; Mismatches 32;
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EMBL, M17838; AAA48704.1; JOINED.
EMBL; VO0401; CAAZ3695.1; -...
EMBL; M10571; AAA48671.1; ALT_SEQ.
EMBL; M17607; AAA48672.1; -...
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TEDINE ON VARIANTS.

MEDLINE=97255959; PubMed=9101290;

Kuivaniemi H., Tromp G., Prockop D.J.;

Kuivaniemi H., Tromp G., Prockop D.J.;

Mutations in fibrillar collagens (types I, II, III, and XI), fibril-associated collagen (type IX), and network-forming collagen (type X) associated collagen (type Done, cartilage, and blood vessels.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Kuivaniemi H., Tromp G., Prockop D.J.; "Mutations in collagen genes: causes of rare and some common diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=86104139; PubMed=3002437;
MEDLINE=86104139; PubMed=3002437;
Nunez A.M., Francomano C., Young M.F., Martin G.R., Yamada Y.;
"Isolation and partial characterization of genomic clones coding for a human pro-alpha 1 (II) colladen chain and demonstration of restriction fragment length polymorphism at the 3' end of the gene.";
Biochemistry 24:6343-6348(1985).
                 MEDLINE-85190534; PubMed=3857598; Cheah K.S.E., Stoker N.G., Griffin J.R., Grosveld F.G., Solomon E.; "Identification and characterization of the human type II collagen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE OF 15-167 FROM N.A.
MEDILINE-89231318; PubMed=2714801;
Su M.W., Benson-Chanda V., Vissing H., Ramirez F.;
"Organization of the exons coding for pro alpha 1(II) collagen N-propertide confirms a distinct evolutionary history of this domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Glycine to serine substitution in the triple helical domain of prapha ! (I) collagen results in a lethal perinatal form of short-limbed dwarfism.";
                                                                                                                                                                                                                   "Construction and identification of a cDNA clone for human type procollagen mRNA.";
Biochem. J. 229:183-188(1985).
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MEDLINE=84118798; PubMed=6320112;
Strom C.M., Upholt W.B.;
Siron and characterion of genomic clones corresponding the human type II procollagen gene.";
Nucleic Acids Res. 12:1025-1038(1984).
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SEQUENCE OF 1120-1398 FROM N.A.
MEDLINE=85306861; PubMed=3940017;
Blima K., Maekelae J.K., Vuorio T., Kauppinen S., Knowles
                                                                                                                                                                                                                                                                                                                 MEDILINE-88067771; Pubmed-2825137;
Elima K., Vuorio T., Vuorio B.;
"Determination of the shaple polyadenylation site of the lapha 1(II) collagen gene.";
Nucleic Acids Res. 15:9499-9504(1987).
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MEDLINE=90036909; PubMed=2572591;
Vissing H., D'Alessio M., Lee B., Ramirez F., Godfrey M., Hollister D.W.;
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Lee B., Vissing H., Ramirez F., Rogers D., Rimoin D.;
"Identification of the molecular defect in a family with
                                                                                                Proc. Natl. Acad. Sci. U.S.A. 82:2555-2559(1985)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Biol. Chem. 264:18265-18267(1989).
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Genomics 4:438-441(1989).
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SEQUENCE OF 963-1418 FROM N.A.
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            GSEGPEGVRGEPGPPGPAGAAGPAGDPGADGEPGAKGADGAPGIAGAPGFPGARGPSGPE
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MEDLINE=90067946; PubMed=2587267;
Su M.W., Lee B., Ramirez F., Machado M., Horton W.;
"Nucleotide sequence of the full length cDNA encoding for human type
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Euteleostomi;
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01-Zhw.1990 (Rel. 13, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
Collagen alpha 1(II) chain precursor [Contains: Chondrocalcin]
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MEDLINE=87031574; PubMed=3021582;
Nunez A.M., Kohno K., Martin G.R., Yamada Y.;
"Promoter region of the human pro-alpha 1(II)-collagen gene.";
Gene 44:11-16(1986).
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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Submitted (DEC-1988) to the EMBL/GenBank/DDBJ databases
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Nucleic Acids Res. 17:9473-9473(1989).
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MEDIINE=93304428; PubMed=8317498; Koerkkoe J., Ritvaniemi P., Haataja L., Kaeaeriaeinen H., Koerkkoe J., Ritvaniemi P., Haataja L., Kaeaeriaeinen H., Kivirikko K.; Prockop D.J., Ala-Kokko L.; Prockop D.J., Ala-Koko L.; Prockop D.J., Ala-Koko L.; Prockop D.J., Ala-Kooliagen (COL2A1) that substitutes aspartate for glycine alpha 1-67 and that causes cataracts and retinal detachment: evidence for molecular heterogeneity in the Wagner Syndrome and the Stickler syndrome (arthro-ophthalmopathy)."; Am. J. Hum. Genet. 53:55-61(1993).
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MEDLINE=92262484; PubMed=1374906;
Horton W.A., Machado M.A., Ellard J., Campbell D., Bartley J.,
Ramirez F., Vitale E., Lee B., Lee
"Characterization of a type II. ollagen gene (COL2A1) mutation
identified in cultured chondrocytes from human hypochondrogenesis.";
Proc. Natl. Acad. Sci. U.S.A. 89:4583-4587(1992).
                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE-91086471, PubMed-1985108;

Eyre D.R., Weis M.A., Moskowitz R.W.;

"Cartilage expression of a type II collagen mutation in an inherited form of osteoarthritis associated with a mild chondrodysplasia.";

J. Clin. Invest. 87:357-361(1991).
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VARIANT SEMD CYS-840.

Tiller G.B., Weis M.A., Lachman R.S., Cohn D.H., Rimoin D.L.,

Fyre D.R.;

"A dominant mutation in the type II collagen gene (COL2A1) produces
spondyloepimeraphyseal dysplasia (SEMD), Strudwick type.";

Am. J. Hum. Genet. 53:A209-A209(1993).
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"Characterization of a type I collagen alpha 2(I) glycine-586 to
valine substitution in osteogenesis imperfecta type IV. Detection (
the mutation and prenatal diagnosis by a chemical cleavage method.
Biochem. J. 276:765-770(1991).
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MEDLINE=93252400; PubMed=8486375;
Vikkula M., Ritvaniemi P., Vuorio A.F., Kaitila I., Ala-Kokko L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=33054548; PubMed-1429602; Bogaert R., Tiller G.E., Wies M.A., Gruber H.E., Rimoin D.L., Cohn D.H., Eyre D.R.; "An amino acid substitution (Gly853-->Glu) in the collagen alpha
                                                                                MEDLINE=90370826; PubMed=1975693; Ala-Kokko L., Baldwin C.T., Moskwwitz R.W., Prockop D.J.; Ala-Kokko L., Baldwin C.T., Moskwwitz R.W., Prockop D.J.; Single base mutation in the type II procollagen gene (COL2A1) cause of primary osteoarthritis associated with a mild chondrodysplasia."; Proc. Natl. Acad. Sci. U.S.A. 87:6565-6568(1990).
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VARIANT OSTEOARTHRITIS CYS-650.
WARDLINE-93282819; PubMed=8507190;
Holderbaum D., Malemud C.J., Moskowitz R.W., Haqqi T.M.;
Holman cartilage from late stage familial osteoarthritis tran
"Human cartilage from late stage familial osteoarthritis tran
type II collagen mRNA encoding a cysteine in position 519.";
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Genomics 16:282-285(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "An amino acid substitution (crycol) 1(II) chain produces hypochondrogenesis."; U. Biol. Chem. 267:22522-22526(1992).
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                                                                                                                                                                                                                                               MEDLINE=91291136; PubMed=2064612;
                                                            NITIS CYS-650.
PubMed=1975693;
oepiphyseal dysplasia.";
244:978-980(1989).
                                                              VARIANT OSTEOARTHRITIS
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spondyloepiphyseal
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Chan D., Taylor T.K.F., Cole W.G.,
"Characterization of an argining 789 to cysteine substitution in
"Characterization of an argining of a patient with spondyloepiphyseal
alpha i (II) collagen chains of a patient with spondyloepiphyseal
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VARIANT SEDC CYS-206.
WARDIANE=94063862; PubMed=8244341;
Williams C.J., Considine E.L., Knowlton R.G., Reginato A., N.
Harrison D., Buxton P., Jimenez S.A., Prockop D.J.,
"Spondyloepiphyeeal dysplasia and precocious osteoarthritis family with an Arg75-->Cys mutation in the procollagen type
                                                                                                                                                                                                Biol. Chem. 268:15238-15245(1993)
                                                                                        Al).";
Genet. 92:499-505(1993)
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Best Local Similarity 71.9
Matches 391; Conservative
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RESULT 6 CA12 MOUSE

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1459 AA; 139154 MW; F6C84FA7C532E7F2 CRC64;
         Missing (in isoform Short)
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OC RATURY COLLAI.

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ON NEBLY TAXID=10116; ROGENTIA; SCIUTOGNATHI; MUTICAL CONTRAINED FOR 1-19.

RY MEDLINES 69155173; PubMed=5777344; RA BOTASTEGIN P.; COMPATATIVE SEQUENCE OF 1-19.

RY The absence of a short sequence at the amino term RT alpha-1 chain.; RL BIOCHEMISTY 8:63-71(1969).

RY MEDLINES 67162268; PubMed=5337886;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                cartilaginous tissues.
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IsoId=228481-2; Sequence=VSP 001139, VSP 001140;
-!- PTM: Prolines at the third position of the tripeptide repeating
unit (G-X-Y) are hydroxylated in some or all of the chains.
-!- SIMILARITY: Contains 1 VWFC domain.
                                                                                                                                                                           Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                              SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.
MEDAINE=91358489; PubMed=1885613;
Metastanta M., Toman D., de Crombrugghe B., Vuorio B.;
Mouse type II collagen gene. Complete nucleotide sequence, exon structure, and alternative splicing.";
J. Biol. Chem. 266:16862-16869(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE OF 1455-1459 FROM N.A.
MEDLINE=91274355; PubMed=2054384;
Metsaranta M., Toman D., de Crombrugghe B., Vuorio E.;
"Specific hybridization probes for mouse type I, II, III and IX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Probom; PD000007; Clg helix; 5.
Probom; PD002078; Fib_collagen_C; 1.
SMART; SM00134; VGF: 1.
SMART; SM00134; VWF: 1; 1.
PROSITE; PS01208; VWFC 1; 1.
PROSITE; PS50164; VWFC 1; 1.
Extracellular matrix; Connective tissue; Repeat; Hydroxylation;
                                   01-DEC-1992 (Rel. 24, Created)
01-DEC-1992 (Rel. 24, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
Collagen alpha 1(II) chain precursor [Contains: Chondrocalcin]
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NONHELICAL REGION (C-TERMINAL).
Q -> R (in isoform Short).
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(BY SIMILARITY).
COLLAGEN ALPHA 1(II) CHAIN.
CHONDROCALCIN.
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EMBL, X57982; CAA41047.1; -.
MGD; MGI.88452; Col2a1.
InterPro; IPR008161; Clg helix.
InterPro; IPR008160; Collagen.
InterPro; IPR00885; Fib_collagen.
InterPro; IPR000885; Fib_collagen.
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Rattus.
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   Length 1459;
Query Match 71.4%; Score 2192; DB 1; Length 1 Best Local Similarity 71.7%; Pred. No. 3.4e-82; Matches 390; Conservative 40; Mismatches 114; Indels
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MEDLINE-72136131; PubMed-4335087;
MEDLINE-72136131; PubMed-4335087;
MELLING J. Click E.M., Bornstein P.;
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Biochemistry 10:4470-4478(1971).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE OF 239-418.
MEDLINE-73006942; PubMed-4342027;
MEDLINE-73006942; PubMed-4342027;
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MEDLINE=6112264; PubMed=6395893;

MEDLINE=6112264; PubMed=6395893;

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Biochemistry 23:6210-6216(1984).

-i- FUNCTION: Type I collagen is a member of group I collagen (fibrillar forming collagen).
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Kang A.H., Bornstein P., Piez K.A.;
"The amino acid sequence of peptides from the cross-linking region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    rat skin
                                                                                                                                                                                       "The incomplete hydroxylation of individual prolyl residues in
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MEDLINE=74011954; PubMed=4126850;
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Eur. J. Biochem. 37:287-294(1973).
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MEDLINE=71263178; PubMed=4327399;
                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE OF 103-139.
MEDLINE=70085124; PubMed=5411206;
                                             rat skin collayen. ,
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                                                                                                                                                                   Bornstein P.;
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its way mon-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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R InterPro; IPRO08161; C1g helix.
R InterPro; IPR008160; Collagen.
R InterPro; IPR0081007; WF C.
R ProDom; PD000007; C1g helix; 1.
R PROSITE; PS01208; WWFC 1; PARTIAL.
W Extracellular matrix; Connective tissue; Repeat; Hydroxylation; Glagen; Pyrrolidome carboxylic acid.
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hydroxyapatite. PTM: Proline residues at the third position of the tripeptide repeating unit (G-X-Y) are hydroxylated in some or all of the
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MEDLINE=7304999; PubMed=4673951;
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"The covalent structure of collagen: amino acid sequence of alpha-1-CB3 from calf skin collagen.";
FEBS Lett. 26:74-76(1972).
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MEDLINE=73042276; PubMed=4343808;
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Bur. J. Blochem. 30:163-168(1972).

-!- FUNCTION: Type I collagen is a member of group I collagen

(fibrillar forming collagen).

-!- SUBUNIT: Trimers of one alpha 2(I) and two alpha 1(I) chains.

-!- TISSUE SPECIFICITY: Forms the fibrils of tendon, ligaments and bydroxyapatite.
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                                                                                                                                                                                                                                                           21-JUL-1986 (Rel. 01, Created)
01-FEB-1994 (Rel. 28, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
Collagen alpha 1(1) chain (Fragments).
                                                                                                                                                                                                                       779 AA
                                                                                                                                                                                                                    PRT;
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SEQUENCE OF 1-19.
MEDLINE=72255334; Pubmed=4115172;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE OF 20-145.
MEDIANE-7602320; PubMed=1164916;
Frietzek P. P., Kuchn K.;
"The covalent structure of collag.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   calf and human collagen.";
Eur. J. Biochem. 27:231-237(1972)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eur. J. Biochem. 30:169-183(1972)
                                    584 GPSGASGPAGPR-----
                                                                              493
                                                                                                                  GPPGPPGPPGPPG 644
                                                                                                                                                                                                                       STANDARD;
                                                                              GPAGPAGPPGPIG
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                                                                              481
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CA11_BOVIN

ID ACCA11_BOVIN

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-!- PTM: Proline residues at the third position of the tripeptide repeating unit (G-X-Y) are hydroxylated in some or all of the chains. Pro-726 is the only 3-hydroxypro and the only hydroxylated proline in position X.
-!- PTM: O-linked glycan consists of a Glc-Gal disaccharide bound to the oxygen atom of a post-translationally added hydroxyl group.
-!- MISCELLANEOUS: The complete chain contains 1052 residues.
PIR; A91193; CGBOIS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            101 GMKGHRGFSGLDGAKGDAGPAGPKGEPGSPGENGAPGQMGPRGLPGFPGPKGAAGEPGKA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    56 GPRGPPGPPGKNGD------DGEAGKPGRPGERGPPGPGAR-----GLPGTAGLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    235 GERGVPGPPGAVGPAGKDGEAGAEGPPGPAGPAGERGEEGPAGSPGFEGLPGPAGPPGEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             295 GKPGEEGVPGDLGAPGPSGARGEPGFPGERGVEGPPGPAGPPGADGAPGDDGAKGDAGAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       355 GAPGSEGAPGLEGMPGERGAAGLPGPKGDRGDAGPKGADGSPGKDGVRGLTGPIGPPGPA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       115 GPTGLPGPPGERGGPGSRGFPGADGVAGPKGPAGERGSPGPAGPKGSPGEAGRPGEAGLP
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                                                                                                                                                                                                                         InterPro; IPR008161; Clg helix.
InterPro; IPR008160; Collagen.
InterPro; IPR001007; VWF C.
ProDom; PD0010007; Clg helix; 1.
PR051TE; PS01208; VWFC 1; PRTIAL.
Extracellular matrix; Connective tissue; Repeat; Hydroxylation;
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                                                                                                                                                                                                                                                                                                                                                                                     Glycoprotein, Collagen, Pyrrolidone carboxylic acid.
MOD_RES 1 1 1 PYRROLIDONE CARBOXYLIC ACID.
MOD_RES 9 9 INVOLVED IN CROSS-LINKING.
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HYDROXYLATION (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                 TISSUE=Aorta;
MEDLINES=88290219; PubMed=9628255;
Shirai T., Hattori S., Sakaguchi M., Inouye S., Kimura A., Ebihara T.,
Irie S., Nagai Y., Hori H.;
"The complete cDNA coding sequence for the bovine proalpha2(I) chain
of type I procollagen."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TISSUE=Skin;
MEDLINE=75008198; PubMed=4412529;
Fietzek P.P., Furthmayr H., Kuehn K.;
"Comparative sequence studies on alpha2-CB2 from calf, human, rabbit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Thetzek P.P., Kuehn K.;

"The covalent structure of collagen: amino acid sequence of the N-
terminal region of alpha2-CB3 from rat skin collagen and alpha2-CB3.

"The covaler skin collagen."

Hoppe-Seyler's Z. Physiol. Chem. 355:647-650(1974).

-- FUNCTION: Type I collagen is a member of group I collagen

(fibrillar forming collagen).

-- SUBUNIT: Trimers of one alpha 2(I) and two alpha 1(I) chains.

-- TISSUE SPECIFICITY: Forms the fibrils of tendon, ligaments and bones. In bones the fibrils are mineralized with calcium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PIM: Prolines at the third position of the tripeptide repeating unit (G-X-Y) are hydroxylated in some or all of the chains.
                                                                                                                                                                                Bos taurus (Bovine).
Nakaryota, Metazoa; Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Cetartiodactyla, Ruminantia, Pecora, Bovoidea,
Bovidae; Bovinae, Bos.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The amino-acid sequence of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=75036115; PubMed=4609475;
Fietzek P.P., Breitkreutz D., Kuehn K.;
"Amino acid sequence of the amino-terminal region of calf skin
         CA21_BOVIN
DCA21_BOVIN
AC P02461
DT 21-JUL-1986 (Rel. 01, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DC COLIA2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Biochim. Biophys. Acta 365:305-310(1974).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Fietzek P.P., Rexrodt F.W.,
"The covalent structure of collagen. T
alpha2-CB4 from calf-skin collagen.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          and pig-skin collagen.";
Eur. J. Biochem. 47:257-261(1974)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE OF 95-415, AND REVISION.
TISSUE=Skin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eur. J. Biochem. 59:113-118(1975)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=76091874; PubMed=173531;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 GSEGPEGVRGEPGPPGPAGAAGPAGDPGADGEPGAKGADGAPGIAGAPGFPGARGPSGPE
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INVOLVED IN CROSS-LINKING (PROBABLE)
HYDROXYLATION (PROBABLE).
HYDROXYLATION (PROBABLE).
HYDROXYLATION (PROBABLE).
HYDROXYLATION (PROBABLE).
HYDROXYLATION (PROBABLE).
HYDROXYLATION (PROBABLE).
EMBL; AB008683; BAA25171.1; -.
InterPro; IPR008161; C1g helix.
InterPro; IPR008160; Collagen.
InterPro; IPR00885; Fib_collagen.
Fem; PF01410; COLF1; 1.
Pfam; PF01410; Collagen; 18.
ProDom; PD000007; C1g helix; 3.
ProDom; PD002078; Fib_collagen_C; 1.
Extracellular matrix; Connective tissue; Repeat; Hydroxylation; Collagen; Signal; Pyrrolidone carboxylic acid.
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llarity 65.3%; Pred. No. 1.9e-72;
Conservative 44; Mismatches 145; Indels 0;
                                                                                                                                                                                                                                                                                                                                                      AMINO-TERMINAL PROPEPTIDE.
COLLAGEN ALPHA 2(1) CHAIN.
CARBOXYL-TERMINAL PROPEPTIDE.
PYROLIDONE CARBOXYLIC ACID.
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K -> T (IN REF. 3).

T -> K (IN REF. 3).

G PGA -> ADP (IN REF. 3).

AT -> TA (IN REF. 3).

129064 MW; 5593F4D6B9ED119A CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=84270666; PubMed=6547770;
Yamada Y., Liau G., Mudryj M., Obici S., de Crombrugghe B.;
"Conservation of the sizes for one but not another class of exons in two chick collagen genes.";
Nature 310:333-337(1984).
                                                                                                                                                                                                                                                                               Nah H.-D., Niu Z., Adams S.L.;
"An alternative transcript of the chick type III collagen gene that does not encode type III collagen.";
J. Biol. Chem. 269:16443-16448 (1994).
                                                                                                                                                                                                                                                                                                                                                 [2] SEQUENCE OF 29-96; 332-397; 431-484; 503-535 AND 869-976 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=83220816; PubMed=6856474;
Yamada Y., Kuhn K., de Crombrugghe B.;
A conserved nucleotide sequence, coding for a segment of the C-propeptide, is found at the same location in different collagen
                            CA13 CHICK STANDARD; PRT; 1262 AA. PI1105; P79758; P9759; Q90794; Q92029; O1-OCT-1989 (Rel. 12, Created) 16-OCT-2001 (Rel. 40, Last sequence update) 28-FB22003 (Rel. 41, Last annotation update) Collagen alpha 1(III) chain precursor (Fragments)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro, IPR008161; Clg helix.
InterPro, IPR008160; Collagen.
InterPro, IPR000885; Fib_collagen_C.
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EMBL, X00822, CAB52686.1; -.
EMBL, X00823, CAB52686.1, J.
EMBL, X00826, CAA25397.1, ALT SEQ.
EMBL, X00825, CAA25397.1, JOINED.
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                                                                                                                                                                                                                                                                     MEDLINE=94266842; PubMed=8206952;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE OF 977-1262 FROM N.A
                                                                                                                                                                                                                                       SEQUENCE OF 1-886 FROM N.A.
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PIR; I50694; I50694
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RESULT 10
CA13_CHICK
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                                                                                                                                                                                                                 SIMILARITY).
TRIPLE-HELICAL REGION (BY SIMILARITY).
NONHELICAL REGION (C-TERMINAL) (BY
                                                                                                                                                                                                     (BY
      InterPro; IPR001007; VWF C.
ProDom; PD00007; Clg_helix; 1.
ProDom; PD000078; Fib_collagen_C; 1.
SMART; SM00214; VWC; 1.
SMART; SM00214; VWC; 1.
PROSITE; PS01208; VWFC 2: 1.
Extracellular matrix; Connective tissue; Repeat; Hydroxylation;
                                                                                                                                                                                                                                                                                                                                                                                                            63.0%; Score 1934.5; DB 1; Length 1262; 63.8%; Pred. No. 7e-72; ive 31; Mismatches 160; Indels 9;
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                                                                                                                                                                   (BY
                                                                                                                                                                                                       NONHELICAL REGION (N-TERMINAL)
                                                                                                                                                                                                                                                                                      INTERCHAIN (BY SIMILARITY).
INTERCHAIN (BY SIMILARITY).
HYDROXYLATION (BY SIMILARITY)
HYDROXYLATION (BY SIMILARITY)
HYDROXYLATION (BY SIMILARITY)
                                                                                                                    POTENTIAL.
AMINO-TERMINAL PROPEPTIDE (BY
                                                                                                                                          SIMILARITY).
COLLAGEN ALPHA 1(III) CHAIN.
CARBOXYL-TERMINAL PROPEPTIDE
                                                                                                                                                                                                                                                                                                                                                                                       96ABE7B2E9DEB43D CRC64;
                                                                                                                                                                                                                                                                                                                                      HYDROXYLATION (BY S. N-LINKED (GLCNAC. E -> K (IN REF. 2). F -> S (IN REF. 3).
                                                                                                                                                                               SIMILARITY)
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InterPro, IPR002181; Fibrinogen_C.
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                                                                                                         Collagen, Signal
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1262
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1003
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96
1132
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145
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283
859
1163
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MOD_RES
MOD_RES
CARBOHYD
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Fietzek P.P., Kuehn K.;
"The covalent structure of collagen: amino acid sequence of the N-terminal region of alpha2-CB3 from rat skin collagen and alpha2-CB3.5 Hoppe-Seyler's Z. Physiol. Chem. 355:647-650(1974).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Fietzek P.P., Piez K.A.; "Independent and characterization of the cyanogen bromide peptides from "Isolation and characterization of the skin collagen."; Biochemistry 8:2129-2133(1969).
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                                                                                                                                                                                                                                                                                                                                                                                                Rattus norvegicus (Rat).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Rattus
NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUE-Skin;
MDDLINE-57162269; PubMed-5337886;
Kang A.H., Bornstein P., Piez K.A.;
"The amino acid sequence of peptides from the cross-linking region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Highberger J.H., Kang A.H., Gross J.;
Comparative studies on the amino acid sequence of the alpha 2-CB2
peptides from chick and rat skin collagens.";
Biochemistry 10:610-616(1971).
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MEDIJINE=73049456; PubMed=4636752;
Fietzek P.P., Kell I., Kuehn K.;
Fietzek P.P., Kell I., Kuehn K.;
Fietzek P.P., Kall I., Kuehn K.;
Fietzek P.P., Kell I., Kell I., Kuehn K.;
Fietzek P.P., Kell I., Kell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
Guenther D., Seibold S., Marx M.;
Submitted (JAN-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                               P02466; Q9R1E8;
21-JUL-1986 (Rel. 01, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Collagen alpha 2(I) chain precursor.
                                                                                                                                                                                                            PRT; 1372 AA
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MEDLINE=75059250; PubMed=4435743;
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MEDLINE=74055004; PubMed=4763308;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            rat skin collagen.";
Biochemistry 6:788-795(1967)
   GPPGPPGPAGKEG 544
                                                    GPPGHPGPAGNNG 911
                                                                                                                                                                                                      STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE OF 423-452.
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532
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COLLAGEN ALPHA 2 (1) CHAIN.
CARBOXYL-TERMINAL PROPEPTIDE

(BY SIMILARITY).
CELL ATTACHNENT SITE (POTENTIAL).
CONVERTED TO AN ALDEHYDE GROUP THAT IS
INVOLVED IN CROSS-LINKING.
N-LINKED (GLCNAC. .) (POTENTIAL).
T -> P (IN REF. 4).
S -> P (IN REF. 4).
S -> P (IN REF. 5).
E -> Z (IN REF. 6).
NISSING (IN REF. 6).
NISSING (IN REF. 6).
NISSING (IN REF. 6).
NISSING (IN REF. 5).
E -> Z (IN REF. 6).
NISSING (IN REF. 5).
R -> K (IN REF. 6).
NISSING (IN REF. 7).
           MEDLINE=10181852; PubMed=5443712;

Vuust J., Lane J.M., Fletzek P.P., Miller E.J., Piez K.A.;

Vuust J., Lane J.M., Fletzek P.P., Miller E.J., Piez K.A.;

"The order of the CNBr peptides from the alpha 2 chain of collagen.";

Plochem. Biophys. Res. Commun. 38:703-708(1970).

-i. FUNCTION: Type I collagen is a member of group I collagen

(fibrillar forming collagen).

-i. SUBUNIT: Trimers of one alpha 2(I) and two alpha 1(I) chains.

-i. TISSUE SPECIFICITY: Forms the fibrils of tendon, ligaments and bones. In bones the fibrils are mineralized with calcium
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 GSEGPEGVRGEPGPPGPAGAAGPAGDPGADGEPGAKGADGAPGIAGAPGFPGARGPSGPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 GPGGPPGPKGDSGEPGAPGSKGDTGAKGEPGPVGVEGPPGPAGEEGKPGARGEPGPTGLP
                                                                                                                                                                                                -!- PTM: Prolines at the third position of the tripeptide repeating unit (G-X-Y) are hydroxylated in some or all of the chains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Extracellular matrix; Connective tissue; Repeat; Hydroxylation; Glycoprotein; Collagen; Signal; Pyrrolidone carboxylic acid. SIGNAL 1 24 POTENTIAL.
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InterPro; IPR008161; Clg helix.
InterPro; IPR008160; Collagen.
InterPro; IPR00885; Fib_collagen_C.
Pfam; PF01410; COLFI; 1.
Pfam; PF01391; Collagen; 18.
ProDom; PD00007; Clg_helix; 4.
ProDom; PD00007; Clg_helix; 4.
ProDom; P0002078; Fib_collagen_C; 1.
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GPTGPVGAAGPSGPNGPPGPAGSRGDGGPPGMTGFPGAAGRTGPPGPSGITGPPGPPGAA
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MEDLINE=85289337; PubMed=2411731;
Medline=85280937; PubMed=2411731;
"Complete primary structure of the human alpha 2 type V procollagen COOH-terminal propeptide.";
J. Biol. Chem. 260:11216-11222(1985).
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MEDLINE=87146331; PubMed=3029669;
MEDLINE=87146331; PubMed=3029669;
Meil D., Bernard M.P., Gargano S., Ramirez F.;
"The pro alpha 2(V) collagen gene is evolutionarily related to the major fibrillar-forming collagens.";
Nucleic Acids Res. 15:181-198(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=89123368; PubMed=2914927; Moodbury D., Benson-Chanda V., Ramirez F.; Manino-terminal propeptide of human pro-alpha 2(V) collagen confor to the structural criteria of a fibrillar procollagen molecule."; J. Biol. Chem. 264:2735-2738(1989).
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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MEDLINE=89138450; PubMed=3224983;
Isipouras P., Schwartz R.C., Liddell A.C., Salkeld C.S., Weil D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-APR-1988 (Rel. 07, Created)
01-JAN-1990 (Rel. 13, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
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SEOUENCE OF 208-227.
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P05997;
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RI "Isolated nof the alpha - Chain of human type V collagen and RI "Isolated nof the alpha - Chain of human type V collagen and Characterization of the alpha - Chain of human type V collagen and Education by Partial sequencing."

RI BIOL. Them. Hoppe-Seyler 331:69-73(1992).

RI SIGNENCE OF 288-297 AND 606-617.

RI MODITIES-922714 his permitted albitag;

READLING-922714 his permitted of the alpha 10." Walland JW." van der Feat W.;

RI JIN SERVILLON BERNILLON J. WALLAND AND AND 60 FEAT W.;

RIN JA BLOCHEN. 221:89-995(1994).

RI DIN JA SERVILLON J. WALLAND OF type V collagen in pair matrix assembly and produce Ribers-Danlos syndrome type I.";

READLING-922717 his permitted in COLSAZ causes Rhier-Danlos syndrome type II.",

READLING-922717 his permitted in COLSAZ causes Rhier-Danlos syndrome type II.",

READLING-922717 his syndrome in COLSAZ causes Rhier-Danlos syndrome type II.",

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                                                 PROSITE; PS01208; VWFC_1; 1.
PROSITE; PS01208; VWFC_2; 1.
EXCASTE: PS50184; VWFC_2; 1.
EXCRECEllular matrix; Connective tissue; Repeat; Hydroxylation; Glycoprotein; Collagen; Signal; Ehlers-Danlos syndrome; Disease mutation; 3D-structure
                                                                                                                                                                                                                                                                   62.6%; Score 1921.5; DB 1; Length 1496; 64.0%; Pred. No. 2.6e-71; .ive 40; Mismatches 153; Indels 3;
                                                                                                               COLLAGEN ALPHA 2(V) CHAIN.
CARBOXYL-TERMINAL PROPEPTIDE.
VWFC.
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HYDROXYLATION.
G -> R (in EDS
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Pfam; PF00093; vwc; 1.
Probom; PD000007; Clg helix; 5.
Probom; PD002078; Fib_collagen_C; 1.
SMART; SM00038; COLFI; 1.
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Matches 348; Conservative
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SEQUENCE TRAIN=C57BL/6J; TISSUE=Mammary gland;

A Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

A Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

A Atschul S.F., Zeeberg B., Buetow K.H., Schefer C.R., Bhat N.K.,

A Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

A Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

A Bapleton M., Soarse M.B., Bonaldo M.F., Carninci P., Prange C.,

A Raba S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Brownstein M.J., Usdin T.B., Toothyuki S., Carninci P., Prange C.,

A Raba S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Brownstein M.J., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

A Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

A Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

A Palakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

Butterfield Y.S.N., Krzywinski M.I., Skalska W., Smailus D.E.,

Butterfield Y.S.N., Krzywinski Of Morre than 15,000 full-length

H. Hong M. Hong M. Marna M.M. Marra M.A.,

H. Hong M. Hong M.M. And M.M. Marra M.A.,

R. Chentartion and initial analysis of more than 15,000 full-length
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MEDILE=2932043; PubMed=1505972;
MEDILE=2932043; PubMed=1505972;

"Sequence analysis of a full-length cDNA for the murine pro alpha
2(1) collagen chain: comparison of the derived primary structure with human pro alpha 2(1) collagen.";

Genomics 13:1345-1346(1992).
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Phillips C.L., Lever L.W., Pinnell S.R., Quarles L.D.,
Wenstrup R.J.;
Construction of a full-length murine pro alpha 2(I) collagen cDNA 1
the polymerase chain reaction.";
J. Invest. Dermatol. 97:980-984(1991).
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Rossi P., de Crombrugghe B.;
Rossi P., de Crombrugghe B.;
Identification of a cell-specific transcriptional enhancer in the first intron of the mouse alpha 2 (type I) collagen gene.";
Proc., Natl. Acad. Sci. U.S.A. 84:5590-5594 (1987).
-!- FUNCTION: Type I collagen is a member of group I collagen (fibrillar forming collagen) 2 (I) and two alpha 1 (I) chains.
-!- SUBUNT: Trimers of one alpha 2 (I) and two alpha 1 (I) chains.
-!- TISSUE SPECIFICITY: Forms the fibrils of tendon, ligaments and bones. In bones the fibrils are mineralized with calcium
                                                                                                                                                                                                                                                                                                Mus musculus (Mouse).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
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Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                    Last sequence update)
Last annotation update)
         Ą
         1372
                                                                             01-APR-1993 (Rel. 25, Created)
16-OCT-2001 (Rel. 40, Last sequence
15-WAR-2004 (Rel. 43, Last annotatio
COLIAGON alpha 2(1) chain precursor.
COLIA2 OR COLA2.
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TISSUE=Calvaria;
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CA21 MOUSE
Q01149;
01-APR-1993 (
16-OCT-2001 (
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[6]
SEQUENCE OF 948-1049.
MEDLINE-80026031; PubMed=488911;
Allmann H., Fietzek P.P., Glanville R.W., Kuhn K.;
Allmann H., Fietzek P.P., Glanville R.W., Kuhn K.;
"The covalent structure of calf skin type III collagen. VI. The amino
acid sequence of the carboxyterminal cyanogen bromide peptide alpha
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE-80026027; PubMed=488907; Dewes H., Fietzek P.P., Kuhn K.; Teersek P.P., Kuhn K.; The amino "The covalent structure of calf skin type III collagen. II. The amino acid sequence of the cyanogen bromide peptide alpha 1(III)CB1,8,10,2 (positions 223-402).";
                                                                                760 GPIGSVGAAGPSGPNGPPGPVGSRGDGGPPGMIGFPGAAGRIGPPGPSGIAGPPGPAA
                                                 GPAGPAGPPGPIGDVGAPGAKGARGSAGPPGATGFPGAAGRVGPPGPSGDAGPPGPPA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "The covalent structure of calf skin type III collagen. I. The amino acid sequence of the amino terminal region of the alpha 1(III) chain (positions 1-222).";
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MEDILINES BROOSCASE, PubMed=488908,
MEDILINES BROOSCASE, PubMed=488908,
Bentz H., Fietzek P.P., Kuhn K.,
"The covalent structure of calf skin type III collagen. III. The
amino acid sequence of the cyanogen bromide peptide alpha 1(III) CB4
(positions 400-551).",
Hoppe-Seyler's Z. Physiol. Chem. 360:833-840(1979).
                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Bovinae; Bos.
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Fietzek P.P., Allmann H., Rauterberg J., Henkel W., Wachter E.,
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MEDLINE=80026030; PubMed=488910;
Dewes H., Fietzek P.P., Kuhn K.;
"The covalent structure of calf skin type III collagen. V. The acid sequence of the cyanogen bromide peptide alpha 1(III)CB9A (position 789-927).";
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Lang H., Glanville R.W., Fietzek P.P., Kuhn K.;
"The covalent structure of calf skin type III collagen: IV. The acid sequence of the cyanogen bromide peptide alpha I(III)CBS (positions 552-788).";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hoppe-Seyler's Z. Physiol. Chem. 360:821-832(1979).
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                                                                                                                                                                                                                                                           20-MAR-1987 (Rel. 04, Created)
20-MAR-1987 (Rel. 04, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Collagen alpha 1(III) chain.
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CONVERTED FO AN ALDEHYDE GROUP THAT INVOLVED IN CROSS-LINKING (BY SIMILARITY).
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Extracellular matrix; Connective tissue; Repeat; Hydroxylation; Glycoprotein; Collagen; Signal; Pyrrolidone carboxylic acid. SIGNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                          (BY SIMILARITY).
COLLAGEN ALPHA 2 (I) CHAIN.
CARBOXYL-TERMINAL PROPEPTIDE
(BY SIMILARITY).
PYRROLIDONE CARBOXYLIC ACID (BY
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V -> A (IN REF. 4).
R -> TT (IN REF. 1).
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EMBL, BC042503, AAR42503.2; -.
EMBL, K01832, AAA37331.1; -.
PIR; A43291, A43291.
InterPro; IPR008161; Clg helix.
InterPro; IPR008161; Clg helix.
InterPro; IPR008161; Clagen.
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Probom; PD002078; Fib_collagen_C; 1.
SMART; SM00038; COLFI; 1.
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Pfam; PF01391; Collagen; 18.
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larity 62.7%; Pred. No. 9.1e-71;
Conservative 36; Mismatches 161; Indels 9;
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TRIPLE-HELICAL REGION.
NONHELICAL REGION (C-TERMINAL).
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"Structure of cDNA clones coding for the entire prepro alpha 1 (III) chain of human type III procollagen. Differences in protein structure from type I procollagen and conservation of codon preferences."; Blochem. J. 260:509-516(1989).
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MEDLINE=79000343; PubMed=687591;
Seyer J.M., Kang A.H.;
"Covalent structure of collagen: amino acid sequence of five consecutive CNBr peptides from type III collagen of human liver.";
Biochemistry 17:3404-3411(1978).
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REVISION TO 1184.
MEDILINE-8909346; PubMed=3211760;
MOlyneux K., Dalgleish R.;
"Human type III collagen 'variant' is a cDNA cloning artefact.";
Nucleic Acids Res. 16:11833-11833 [1988).
                                                                                                                                                                                                                                                                                                                                                                                                            Euteleostomi;
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MEDLINE=77134724; PubMed=557335;
Seyer J.M., Kang A.H.;
"Covalent structure of collagen: amino acid sequence of cyanogen bromide peptides from the amino-terminal segment of type III coll
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MEDLINE-89350838; PubMed-2764886;
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01-UAN-1990 (Rel. 13, Last sequence update)
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Collagen alpha 1(III) chain precursor.
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MEDLINE=89386015; PubMed=2780304;
Janeczko R.A., Ramirez F.;
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Submitted (DEC-1977) to the PIR
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744 GKDGPPGPPGSNG 756
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MEDLINB=85157600; PubMed=2579949;
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SEQUENCE OF 1065-1466 FROM N.A.
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"Molecular cloning and carboxyl-propeptide analysis of human type III
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MEDLINE-93293988; PubMed-8514866;

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MEDLINE=88303360; PubMed=3405773;
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MEDLINE=94016385; PubMed=8411057;
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VARIANT EDS-1V VAL-960.
WARIANT EDS-1V VAL-960.
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MEDLINE-92316511; PubMed-1352273;
Richards A.J., Ward P.N., Narcisi P., Nicholls A.C., Lloyd J.C.,
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Richards A.J., Lloyd J.C., Ward P.N., de Paepe A., Narcisi P.,
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Johnson P.H., Richards A.J., Pope F.M., Hopkinson D.A.;
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qq	480 GAAGERGAPGFRGPAGPNGIPGEKGPAGERGAPGPAGPRGAAGEPGRDGVPGGPGMRGMP 539
δ	181 GSEGSPGPDGKTGPPGPAGEDGRPGPPGPRGBAGWMGFPGPKGAAGEPGKAGERGVP 240
Ωp	540 GSPGGPGSDGKPGPPGSQGESGRPGPPGPSGPRGQPGVWGFPGPKGNDGAPGKNGERGGP 599
à	241 GPPGAVGPAGKDGEAGAEGPPGPAGPAGERGEEGPAGSPGFEGLPGPAGPPGEAGKPGEE 300
qq	600 GGPGPQGPPGKNGETGPQGPPGPGGDKGDTGPPGPQGLQGLPGTGGPPGENGKPGEP 659
ò	301 GVPGDLGAPGPSGARGEPGFRGVEGPPGPPGADGAPGDDGAKGDAGAPGAP 357
q	660 GPKGDAGAPGGRGDAGAPGERGPPGLAGAPGLRGGAGPPGPPGGRGAAGPPGPP 716
ò	358 GSECAPGLEGMPGERGAAGLPGPKGDRGDAGPKGADGSPGKDGVRGLTGPIGPPGPAGAP 417
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'n	478 GPPGPAGPAGPPGDLGDVGAPGARGSAGPPGATGFPGAAGRVGPPGPSGDAGPPGPP 537
q	837 GPPGVAGPPGGSGPAGPPGPQGVKGERGSPGGPGAAGFPGARGLPGPPGSNGNPGPPGPS 896
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1: geneseqp1980s:*

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SUMMARIES

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ALIGNMENTS

Extracellular matrix protein; self aggregation; hydroxylated proline; trans-4-hydroxyproline; 3-hydroxyproline; recombinant protein production; collagen; fibrinogen; fibronectin; post translational hydroxylation. Amino acid sequence of a human collagen 1 (alpha1) protein. AAY84541 standard; protein; 1057 AA (first entry) 25-JUL-2000 AAY84541;

Homo sapiens.

EP992586-A2.

12-APR-2000.

99EP-00119184. 07-OCT-1999; 98US-00169768. 09-OCT-1998;

(USSU) US SURGICAL CORP.

Connolly K; Gruskin EA, Buechter DD, Zhang G,

WPI; 2000-259138/23. N-PSDB; AAA12502.

Production of extracellular matrix proteins containing 4-trans-hydroxyproline results in native self aggregating proteins, useful on medical implants.

Disclosure; Fig 27A-E; 260pp; English.

The specification describes a method for producing an extracellular matrix protein or its fragment. The extracellular matrix protein is expable of self aggregating in a cell which does not ordinarily hydroxylated prolines. The method comprises optimising a nucleic acid sequence for expression in the cell by substitution of codons preferred by that cell for naturally occurring codons not preferred by the cell; in corporating the nucleic acid sequence into the cell; and contacting the corporating the nucleic acid sequence into the cell; and contacting the cell with a hypertonic growth medium containing at least one amino acid, selected from the group consisting of trans 4-hydroxyproline and acid, selected from the group consisting of trans 4-hydroxyproline and 3-into the cell and incorporated into the extracellular matrix protein. The

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Production of extracellular matrix proteins containing 4-trans-hydroxyproline results in native self aggregating proteins, useful

Example 10; Fig 39A-E; 260pp; English

medical implants.

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Connolly

Zhang G,

Buechter DD,

Gruskin EA,

2000-259138/23.

N-PSDB; AAA12503

(USSU) US SURGICAL CORP

99EP-00119184 98US-00169768

07-OCT-1999; 09-0CT-1998;

EP992586-A2

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method may be used to make host cells assimilate and incorporate trans-4-
hydroxyproline into proteins. This is especially useful in the
recombinant production of proteins such as colladen, fibrinogen and
fibronectin whose ability to self aggregate and produce functional
proteins depends on the post translational hydroxylation of proline. The
method is also useful in studying the structure and function of
polypeptides which do not normally contain trans-4-hydroxyproline. The
present sequence represents a human collagen i (alphal) protein, which
may be produced using the method of the invention
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                                                                                                                                                                                                 96.6%; Score 2966; DB 3;
95.6%; Pred. No. 2.7e-169;
ive 21; Mismatches 3;
                                                                                                                                                                                                                  Local Similarity 95.6 es 520; Conservative
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The specification describes a method for producing an extracellular matrix protein or its fragment. The extracellular matrix protein is capable of self aggregating in a cell which does not ordinarily hydroxylated prolines. The method comprises optimising a nucleic acid sequence for expression in the cell by substitution of codons preferred by that cell for naturally occurring codons not preferred by the cell; in corporating the nucleic acid sequence into the cell; and contacting the cell with a hypertonic growth medium containing at least one amino acid, selected from the group consisting of trans-4-hydroxyproline and 3-chydroxyproline to allow at least one of the amino acids to be assimilated into the cell and incorporated into the extracellular matrix protein. The method may be used to make host cells assimilate and incorporate trans-4-hydroxyproline into proteins. This is especially useful in the recombinant production of proteins such as collagen, fibrinogen and fibronectin whose ability to self aggregate and produce functional proteins depends on the post translational hydroxyproline. The method is also useful in studying the structure and function of proteins expensents shown as collagen. (alphal) helical region, chieful and contains dependence represents human collagen; captain and produce function of presents expense the sequence in the contains trans-4-hydroxyproline. The contains dependence represents human collagen; captain in studying the structure and function of presents expensents human collagen; captain in the contains dependence represents human collagen; captain in the contains dependence represents and produce function of presents expensed the contains dependence represents and captains in the contains dependence represents the sequence in the contains the contains dependence represents and captains in the contains dependence represents and captains in the contains the contains dependence represents the contains the contains dependence represents the contains the contains the contains the con
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Matches 520;
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Extracellular matrix protein; self aggregation; hydroxylated proline; trans-4-hydroxyproline; 3-hydroxyproline; recombinant protein production; collagen; fibrinogen; fibronectin; post translational hydroxylation.

Homo sapiens

A human collagen 1 (alpha1) protein helical region.

(first entry)

25-JUL-2000

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AAY84544 standard; protein; 1057

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01-OCT-1996
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Key
Domain
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  Matches
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AAR89472
                                                                                                                                                                                                                                                                                                                                                                                                                                                              ద
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present sequence represents a human type 1 (alphal) collagen protein. Peptides derived from the protien were used to demonstrate incorporation of 3,4-dehydro---prolline into the peptide, using the method of the invention. The specification describes a method for the incorporation of non-natural amino acid into a polypeptide. The method comprises reacting at least one 3,4-dehydroprolline residue in the polypeptide with an epoxyprolline residue. The method is used for studying the effects of non-natural amino acids on structure and function of polypeptides. The method is also wiseful for commercial production of collagen or mussel adhesive proteins (which are useful as bloadbesives), and for incorporating a wide variety of groups, including therapeutic ligands and biological probes,
                                                                       480
                                                                                                                 680
                                                                                                                                                                540
                                                                                                                                                                                           GPAGPAGPPGPIGNVGAPGAKGARGSAGPPGATGFPGAAGRVGPPGPSGNAGPPGPPGPA 740
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Alphal collagen; 3,4-dehydro-L-proline; epoxidation; 3,4-epoxyproline; collagen; mussel adhesive protein; bioadhesive.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     for
                        GAPGLQGMPGERGAAGLPGPKGDRGDAGPKGADGSPGKDGVRGLTGPIGPPGPAGAPGDK
                                                                                                                                                           GPAGPAGPPGPIGDVGAPGAKGARGSAGPPGATGFPGAAGRVGPPGPSGDAGPPGPPGPP
                                                                                                              GESGPSGPAGPTGARGAPGDRGEPGPPGPAGPPGADGQPGAKGEPGDAGAKGDAGPP
                                                                     GESGPSGPAGPTGARGAPGDRGEPGPPGPAGFAGPPGADGEPGAKGEPGDAGAKGDAGPP
Incorporating non-natural amino acid into polypeptide, useful e.g. production of bioadhesives, by epoxidation or substitution of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                type 1 (alpha1) collagen polypeptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 1058;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 2966; DB 3;
Pred. No. 2.7e-169;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Buechter
                                                                                                                                                                                                                                                                                                                                                                                                                    AAY84403 standard, protein, 1058 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; Fig 6; 66pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Amino acid sequence of human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 98US-0099652P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         99WO-US020462.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    96.6%;
95.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gruskin EA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (USSU ) US SURGICAL CORP. (PAOL/) PAOLELLA D N. (GRUS/) GRUSKIN E A. (BUEC/) BUECHTER D D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            dehydroproline residues.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2000-271051/23.
N-PSDB; AAZ99843.
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Best Local Similarity
                                                                                                                                                                                                                                                                                                  744
                                                                                                                                                                                                                                                      GKEG 544
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 1058 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO200014201-A1
                                                                                                                                                                                                                                                                                                     GKEG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens
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AAY8403
AAY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  682 GPAGPPGPIGNVGAPGAKGARGSAGPPGATGFPGAAGRVGPPGPSGNAGPPGPPGPA
                                                                      202 GSEGPQGVRGEPGPPGPAGPAGPAGNPGADGQPGAKGANGAPGIAGAPGFPGARGPSGPQ
                                                                                                                                                                                                                                                                                                                                                                                                       GVPGDLGAPGPSGARGEPGFPGERGVEGPPGPAGPPGADGAPGDDGAXGDAGAPGAPGSE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GESGPSGPAGPTGARGAPGDRGEPGPPGPAGFAGPPGADGEPGAKGEPGDAGAKGDAGPP
                                    1 GSEGPEGVRGEPGPPGPAGAAGPAGDPGADGEPGAKGADGAPGIAGAPGFPGARGPSGPE
                                                                                                           GPGGPPGPKGDSGEPGAPGSKGDTGAKGEPGPVGVEGPPGPAGEEGKPGARGEPGPTGLP
                                                                                                                                262 GPGGPPGPKGNSGEPGAPGSKGDTGAKGEPGPVGVQGPPGPAGEEGKRGARGEPGPTGLP
                                                                                                                                                                                 121 GPPGERGGPGSRGFPGADGVAGPKGPAGERGSPGPAGPKGSPGEAGRPGEAGLPGAKGLT
                                                                                                                                                                                                                GPPGERGGPGSRGFPGADGVAGPKGPAGERGSPGPAGPKGSPGEAGRPGEAGLPGAKGLT
                                                                                                                                                                                                                                                         GSPGSPGPDGKTGPPGPAGEDGRPGPPGPPGARGEAGVMGFPGPKGAAGEPGKAGERGVP
                                                                                                                                                                                                                                                                                          GSPGSPGPDGKTGPPGPAGQDGRPGPPGPPGARGQAGVMGFPGPKGAAGEPGKAGERGVP
                                                                                                                                                                                                                                                                                                                                 GPPGAVGPAGKDGEAGAEGPPGPAGPAGERGEEGPAGSPGFEGLPGPAGPPGEAGKPGEE
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Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Transforming growth factor, TGF-beta-1; collagen IA; osteogenesis; bone formation; tissue repair; fusion protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1058. .1059
|Tabel= Linker_peptide
|1060. 11007
|Tabel= Decorin
|note= "amino acids P46 to G93 of mature decorin"
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/label= Collagen-IA
/note= "collagen IA alpha-helical domain"
Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     note= "unidentified amino
21; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Collagen/decorin(aa46~93) fusion protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAR89472 standard; protein; 1107 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
 Conservative
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Sequence 1107 AA;
                                                                                                                                                                                                                                                                                                                                       Chimeric
                                                             RESULT 5
                                                                             AAY84540
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                                                                                                                                                                                                          Chimaeric DNA encoding protein contg. extracellular matrix protein domain - and cellular regulatory factor domain, partic. useful as osteogenic agents, also related vectors, transformed cells and chimaeric proteins.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9
                                                                                                                                                                                                                                                                                                   A fusion protein (AAR89472) comprises the alpha-helical region of human collagen I(a) linked to amino acids 46-93 of human mature dermatan sulphate proteoglycan (decorin). It can be expressed in Escherichia collaransformants carrying a vector incorporating a chimeric gene (AAR16518) coding for the fusion. The decorin binds to type I collagen and thus affects Elbril formation. It inhibits the cell attachment-promoting activity of collagen and fibrinogen by binding to such molecules near their cell binding sites. The collagen moiety provides an integral substratum or scaffolding for the decorin. The fusion protein acts to reduce scarring of healing tissue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 GSEGPEGVRGEPGPPGPAGAAGPAGDPGADGEPGAKGADGAPGIAGAPGFPGARGPSGPE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 1107;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  96.6%; Score 2966; DB 2;
95.6%; Pred. No. 2.8e-169;
tive 21; Mismatches 3;
                                                                                                                                                                                                                                                                         Disclosure; Fig 8; 59pp; English
                             95CA-02151547
                                                             94US-00259263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                            (USSU ) US SURGICAL CORP
                                                                                                                            Espino P;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
Matches 520; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 1107 AA;
                                                                                                                                                                         N-PSDB; AAT16518
                              12-JUN-1995;
                                                             10-JUN-1994;
11-DEC-1995
                                                                                                                            Gruskin EA,
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The specification describes a method for producing an extracellular matrix protein is matrix protein or its fragment. The extracellular matrix protein is capable of self aggregating in a cell which does not ordinarily hydroxylated prolines. The method comprises optimising a nucleic acid sequence for expression in the cell by substitution of codons preferred by that cell for naturally occurring codons not preferred by the cell; incorporating the nucleic acid sequence into the cell; and contacting the incorporating the nucleic growth medium containing at least one amino acid, selected from the group consisting of trans-4-hydroxyproline and 3-hydroxyproline to allow at least one of the amino acids to be assimilated into the cell and incorporated into the extracellular matrix protein. The method may be used to make host cells assimilate and incorporate trans-4-hydroxyproline into proteins. This is especially useful in the hydroxyproline into proteins such as collagen, fibrinosgen and fibronectin whose ability to self aggregate and produce functional contains depends on the post translational hydroxylation of proline. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Extracellular matrix protein; self aggregation; hydroxylated proline; trans-4-hydroxyproline; 3-hydroxyproline; recombinant protein production; collagen; fibrinogen; fibronectin; post translational hydroxylation;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Amino acid sequence of a chimeric collagen 1 (alpha1)/decorin protein.
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This invention relates to novel nucleic acids and proteins present in normal and neoplastic pancratic calls, pancratic cancer is a common cause of cancer death worldwide, therefore accurate methods of diagnosis and treatment are required. Compounds which modulate the proteins of the invention may have cytostatic activity and the protein and DNA sequences of the invention may be useful for the development of a vaccine or in gene therapy. The composition and methods are useful in diagnosing, staging, inaging, monitoring, preventing or treating pancreatic cancer and non-cancerous disease states of the pancreas. The present sequence is that of a human pancreatic protein of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            98US-00169768,
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Unidentified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            09-OCT-1998;
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                                                                                                                                                                                                                                                                                                                                                                        25-JUL-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                Chimaeric DNA encoding protein contg. extracellular matrix protein domain - and cellular regulatory factor domain, partic. useful as osteogenic agents, also related vectors, transformed cells and chimaeric proteins.
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                               Bone morphogenic protein 2B; BMP-2B; collagen IA; osteogenesis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 1169;
                                                                                                   1. .1057
/label= Collagen-IA
/note= "collagen IA alpha-helical domain"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    96.6%; Score 2966; DB 2;
95.6%; Pred. No. 2.9e-169;
tive 21; Mismatches 3;
                                                                                                                                                 'note= "unidentified amino acid"
                                                                                                                                                                       amino acid"
                                                                                                                                                                                 1058. .1059
|/label= Linker_peptide
|1060. .1169
|/label= BMP-2B
|/note= "human mature BMP-2B"
                                                                                                                                                                      'note= "unidentified
                                                                                          location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure, Fig 5, 59pp, English.
           Collagen/BMP-2B fusion protein.
                                                                                                                                                                                                                                                                                                        95CA-02151547
                                                                                                                                                                                                                                                                                                                              94US-00259263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 95.6%
Matches 520; Conservative
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                                                                                                                                      Misc-difference
                                                                                                                                                             Misc-difference
                                              fusion protein.
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                                                                   Synthetic
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trans-4-hydroxyproline; 3-hydroxyproline; recombinant protein production; collagen; fibrinogen; fibronectin; post translational hydroxylation; ss. bone morphogenic protein; BMP-2B; chimera.
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hydroxyproline results in native self aggregating proteins, useful on
medical implants.
Extracellular matrix protein; self aggregation; hydroxylated proline;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ë
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note= "unspecified amino acid encoded by CT"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Connolly
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us-10-658-989a-4.rag

(first entry) 01-OCT-1996

Collagen/TGF-beta-1 fusion protein.

collagen IA; osteogenesis; Transforming growth factor; TGF-beta-1; collar bone formation; tissue repair; fusion protein

Synthetic

Location/Qualifiers 1. 1057 /label= Collagen-IA /note= "collagen IA alpha-helical Key Domain

887 Misc-difference

domain"

'note= "unidentified amino acid" 'note= "unidentified amino Misc-difference

1058. 1059 | Jabel= Linker_peptide | 1060. 1171 | Jabel= TGF-beta-1 | Jobe= "human mature TFF-beta-1" Peptide

Sequence 1169 AA;

CA2151547-A.

95CA-02151547. 12-JUN-1995;

94US-00259263 (USSU) US SURGICAL CORP. 10-JUN-1994;

Espino P; Gruskin EA,

WPI; 1996-140144/15. N-PSDB; AAT16516.

Chimaeric DNA encoding protein contg. extracellular matrix protein doma - and cellular regulatory factor domain, partic. useful as osteogenic agents, also related vectors, transformed cells and chimaeric proteins.

Disclosure; Fig 6; 59pp; English

A fusion protein (AAR89470) comprises the alpha-helical region of human collagen I(a) linked to the human mature transforming growth factor beta-(iTGF-beta-1). It can be expressed in Escherichia coli transformants carrying a vector incorporating a chimeric gene (AAT16516) coding for the fusion. The TGF-beta-motety increases efficacy of the body's normal soft tissue repair response and also induces osteogenesis. The collagen moiety provides an integral substratum or scaffolding for the TGF and cells involved in reconstruction and growth. The fusion protein provides sustained release and delivery of TGF-beta-1 to a target tissue

Sequence 1171 AA;

Gaps ô Length 1171; 3; Indels 96.6%; Score 2966; DB 2; 95.6%; Pred. No. 2.9e-169; ive 21; Mismatches 3; Query Match Best Local Similarity 95.6 Matches 520, Conservative

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260 201 GSEGPQGVKGEPGPPGPAGAAGPAGNPGADGQPGAKGANGAPGIAGAPGFPGARGPSGPQ GSEGPEGVRGEPGPPGPAGAAGPAGDPGADGEPGAKGADGAPG1AGAPGFPGARGPSGPE

> 셤 8 g à

180 GPPGERGGPGSRGFPGADGVAGPKGPAGERGSPGPAGPKGSPGEAGRPGEAGLPGAKGLT 121

440 180 380 240 480 540 260 GPGGPPGPKGDSGEPGAPGSKGDTGAKGEPGPVGVEGPPGPAGEEGKPGARGEPGPTGLP 120 GPPGAVGPAGKDGEAGAEGPPGPAGERGEEGPAGSPGFEGLPGPAGPPGEAGKPGEE 300 500 GVPGDLGAPGPSGARGEPGFPGERGVEGPPGPAGPPGADGAPGDDGAKGDAGAPGAPGSE 360 560 GAPGLEGMPGERGAAGLPGPKGDRGDAGPKGADGSPGKDGVRGLTGPIGPPGPAGAPGDK 420 GESGPSGPAGPTGARGAPGDRGEPGPPGPAGPAGPPGADGQPGAKGEPGDAGARGDAGPP 680 GPAGPAGPPGPPGNVGAPGAKGARGSAGPPGATGFPGAAGRVGPPGPSGNAGPPGPPGPA 740 GAPGLOGMPGERGAAGLPGPXGDRGDAGPKGADGSPGKDGVRGLTGPIGPPGPAGAPGDK 620 9 GPGGPPGPKGNSGEPGARGETGENGETGEPGPVGVQGPPGPAGEEGKKGARGEFGPTGLP GSPGSPGRDGKTGPPGPAGQDGRPGPPGARQQAGVMGFPGPKGAAGEPGKAGERGVP GPPGAVGPAGKDGEAGAQGPPGPAGPAGERGEQGPAGSPGFQGLPGPAGFPGEAGKPGEQ 1 GSEGPEGVRGEPGPPGPAGAAGPAGDPGADGEPGAKGADGAPGIAGAPGFPGARGPSGPE GPPGERGGPGSRGFPGADGVAGPKGPAGERGSPGPAGPKGSPGEAGRPGEAGLPGAKGLT GPPGERGGPGSRGFPGADGVAGPKGPAGERGSPGPAGPKGSPGEAGRPGEAGLPGAKGLT GSPGSPGPDGKTGPPGPAGEDGRPGPPGPPGARGEAGVMGFPGPKGAAGEPGKAGERGVP GESGPSGPAGPTGARGAPGDRGEPGPPGPAGFAGPPGADGEPGAKGEPGDAGAKGDAGPP GPAGPAGPPGPIGDVGAPGAKGARGSAGPPGATGFPGAAGRVGPPGPSGDAGPPGPPGPA Gaps .; 0 96.6%; Score 2966; DB 3; Length 1169; 95.6%; Pred. No. 2.9e-169; cive 21; Mismatches 3; Indels 0 Conservative Similarity 744 **GKEG 544** GKEG Best Local Simi Matches 520; 261 321 561 201 61 181 381 241 441 501 361 621 481 581 541 Query Match Best Local 121 301 421 741 셤 δ 음 성 음 g 원 8 음 q \$ 8 \$ δ à ò 음 8

AAR89470 standard; protein; 1171 AA. RESULT 9 AAR89470 ID AAR89

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Claim 23; Fig 15; 260pp; English
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Best Local Similarity 95.6
Matches 520; Conservative
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hydroxyproline results in native self aggregating proteins, useful on
medical implants.
                                                                                            GSPGSPGPDGKTGPPGPAGEDGRPGPPGPPGARGEAGVMGPPGPKGAAGEPGXAGERGVP
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capable of self aggregating in a cell which does not ordinarily capable of self aggregating in a cell which does not ordinarily capable of self aggregating in a cell which does not ordinarily capable of sequence for expression in the cell by substitution of codons preferred by that cell for naturally occurring codons not preferred by the cell; incorporating the nucleic acid sequence into the cell; and contacting the cell with a hypertonic growth medium containing at least one amino acid, selected from the group consisting of trans-4-hydroxyproline and 3-chydroxyproline to allow at least one of the amino acids to be assimilated into the cell and incorporated into the extracellular matrix protein. The method may be used to make host cells assimilate and incorporate trans-4-hydroxyproline into proteins. This is especially useful in the recombinant production of proteins such as collagen, fibrinogen and fibronectin whose ability to self aggregate and produce functional corputation also useful in studying the structure and function of proteins expensents enthemory that explained the produced using the prowth factor-betal (TGF-betal) protein, which may be produced using the method of the invention
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specification describes a method for producing an extracellular
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New pancreatic specific nucleic acid molecule or protein for diagnosing, staging, imaging, monitoring, preventing or treating pancreatic cancer onn-cancerous disease states of the pancreas.
GAPGLEGMPGERGAAGLPGPKGDRGDAGPKGADGSPGKDGVRGLTGPIGPPGPAGAPGDK
                                                                 GESGPSGPAGPTGARGAPGDRGEPGPPGPAGFAGPPGADGEPGAKGEPGDAGAKGDAGPP
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larity 95.6%; Pred. No. 3e-169;
Conservative 21; Mismatches 3;
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N-PSDB; ADE87403.
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95.6%; Pred. No. 3e-169;
ive 21; Mismatches 3; Indels
                                                                                            Human pancreatic cell protein sequence SeqID517.
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 standard; protein; 1211
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Best Local Similarity 95.6%
Matches 520; Conservative
                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                (DIAD-) DIADEXUS INC
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N-PSDB; ADE87397.
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                                                                                                                                                                                                                                                                                                                                                                                  Liu C;
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A fusion protein (AAR89471) comprises the alpha-helical region of human collagen I(a) linked to human dermatan sulphate proteoglycan (decorin). It can be expressed in Escherichia coli transformante carrying a vector incorporating a chimeric gene (AAT16517) coding for the fusion. The decorin binds to type I collagen and thus affects Elbril formation. It inhibits the cell attachment-promoting activity of collagen and this fibrinogen by binding to such molecules near their cell binding sites. The collagen moiety provides an integral substratum or scaffolding for the decorin. The fusion protein acts to reduce scarring of healing tissue
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.larity 95.6%; Pred. No. 3.4e-169;
Conservative 21; Mismatches 3;
                                                                                                                                                                                                                                                             Disclosure; Fig 7; 59pp; English
               95CA-02151547
                                              94US-00259263
                                                                              (USSU ) US SURGICAL CORP
                                                                                                               Espino
                                                                                                                                              1996-140144/15.
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Best Local Similarity
Matches 520; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 1388 AA;
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               12-JUN-1995;
                                                                                                               Gruskin EA,
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             GSEGPEGVRGEPGPPGPAGAAGPAGDPGADGEPGAKGADGAPGIAGAPGFPGARGPSGPE
                                 GSEGPQGVRGEPGPPGPAGAAGPAGNPGADGQPGAKGANGAPGIAGAPGFPGARGPSGPQ
                                                                                                                                                                                                             GSPGSPGPDGKTGPPGPAGEDGRPGPPGPPGARGEAGVMGFPGPKGAAGEPGKAGERGVP
                                                                                                                                                                                                                                GSPGSPGKTGPPGPAGDGRPGPPGPPGARGQAGWGFPGPKGAAGEPGKAGERGVP
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                                                                              GPGGPPGPKGDSGEPGAPGSKGDTGAKGEPGPVGVEGPPGPAGEEGKPGARGEPGPTGLP
                                                                                                             GPGGPPGPKGNSGEPGAPGSKGDTGAKGEPGPVGVQGPPGPAGEEGKRGARGEPGPTGLP
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                                                                                                                                                                             GPPGERGGPGSRGFPGADGVAGPKGPAGERGSPGPAGPKGSPGEAGRPGEAGLPGAKGLT
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1. .1057
/label= Collagen-IA
/note= "collagen IA alpha-helical domain"
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/label= Linker_peptide
1060. .1388
/label= Decorin
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890
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718 420 778 480 838 540

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us-10-658-989a-4.rag

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GVPGDLGAPGPSGARGEPGFFGERGVEGPPGPAGPPGADGAPGDDGAKGDAGAPGAPGSE 360
                 GSPGSPGFDGKTGPPGPAGQDGRPGPPGARGQAGVMGFPGPKGAAGEPGKAGERGVP
                                                                         599 GPPGAVGPAGKDGEAGAQGPPGPAGPAGERGEQGPAGSPGFQGLPGPAGPPGEAGKPGEQ
                                                                                                                                     GVPGDLGAPGPSGARGERGFPGERGVQGPPGPAGPRGANGAPGNDGAKGDAGAPGAPGSQ
                                                                                                                                                                                               GAPGLQGMPGERGAAGLPGPKGDRGDAGPKGADGSPGKDGVRGLTGPIGPIGPPGPAGAPGDK
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The method comprises: (a) culturing a recombinant host cell comprising a constant of a fibrillar collagen monomer lacking a C propertide SSAD (sequence selection and alignment domain); and (b) producing the fibrillar collagen. The methods are used to produce fibrillar collagen, comprising DNA encoding a collagen fibrils can be derived. Host cells, comprising DNA encoding a collagen monomer lacking SSAD or N propeptide is used to produce gelatin. Collagen is used in biological research as a substrate for in vitro cell culture and as a component of biocompatible matrices, artificial skin and wound dressing and healing devices. Gelatin is particularly useful for foodstuffs and medicine, for coating tablets and making capsules. The methods, comprising the use of collagen monomers lacking the N and/or C propeptides, result in a large increase in the production of type I collagen. He present sequence represents the human preproalpha I (I) collagen (GenBank Accn no: AP017178)
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                                                                                                                                                                           Fibrillar collagen; C propeptide; SSAD; telopeptide; gelatin; sequence selection and alignment domain; prosthetic implant; foodstuff; medicine; type I collagen; human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   419 GPGGPPGPKGNSGEPGAPGSKGDTGAKGEPGPVGVQGPPGPAGEEGKRGARGEPGPTGLP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New method for production of fibrillar collagen, useful for preparing telopeptide collagen fibrils and gelatin.
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96.6%; Score 2966; DB 3;
Best Local Similarity 95.6%; Pred. No. 3.4e-169;
Matches 520; Conservative 21; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                   Chisholm GE;
                                                          AAY56800 standard; protein; 1411 AA.
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                                                                                                                                                  Human preproalpha 1 (I) collagen.
                                                                                                                                                                                                                                                                                                                                                         98US-0084828P.
99US-00289578.
                                                                                                                                                                                                                                                                                                                               99EP-00303470.
                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                   Hitzeman RA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2000-074666/07.
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                                                                                                                                                                                                                                        Homo sapiens
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                                                                                                                    27-MAR-2000
                                                                                                                                                                                                                                                                                                                             04-MAY-1999;
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                               RESULT 14
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Stimulating or inhibiting cell growth and/or division, useful for
stimulating chondrogenesis, cartilage, disc or connective tissue growth,
repair, and/or regeneration, comprises administering deer antler
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                                                                                                                                                                                                                                                                                                                                                                                                    Human, deer, rat, mouse, DACC, deer antler cartilage cell; cell stimulation; cell inhibition; cell growth; cell division; mesenchymal cell; chondrocyte; chondrogenesis; osteogenesis; growth; repair; regeneration; restoration; extracellular matrix; cartilaginous matrix; cartilaginous matrix; cartilage; disc; connective tissue; agonist; antagonist; gene therapy.
                                                                                                                                                                                                                                                                                                                 Human polypeptide orthologous to DACC-11.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 13; Page 154-160; 214pp; English.
ABG93947 standard; protein; 1461 AA
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cert Unactor formers assertable and characterity, the method relates to these polypeptides capable of stimulating chondrogenesis, the genes of these polypeptides capable of stimulating chondrogenesis, the genes of these polypeptides capable of stimulating chondrogenesis, osteogenesis, growth, repair, regeneration and/or restoration of the extracellular matrix. The DACC polypeptides and polymocleotides are useful for identifying an agent that modulates the activity of the polypeptide, for stimulating mesenchymal cell growth and/or division by exposing animal mesenchymal cell growth and/or division by exposing animal mesenchymal cell growth and/or division by exposing animal mesenchymal cells to conditioned media or its active fraction, obtained from deer antler cartilage cells, for inhibiting cell growth and/or division by inserting into an animal cell, a compound which inhibits the translation of the polypucleotide encoding the DACC. The method and the polypeptides are useful for stimulating mesenchymal cell growth and/or division or for stimulating chondrogenesis, cartilage, disc or connective tissue growth, repair, regeneration and/or restoration in growth and/or division or for stimulating chondrogenesis, cartilage, disc or connective tissue growth, repair, regeneration and/or restoration in glowthead in treatment modalities, specifically in gene therapy. The polypoptides can be used as bait proteins in a two- or three-hybrid assay to polypeptide and are involved in modulating cell growth and/or division. The sequences presented in ABG99923-ABG9948 are the proteins encoded by the DACC cDNA clones ô 538 420 598 GPGGPPGPKGDSGEPGAPGSKGDTGAKGEPGPVGVEGPPGPPGBEGKPGARGEPGPTGLP 120 419 GPGGPPGPKGNSGEPGAPGSKGDTGAKGEPGPVGVQGPPGPAGEBGKRGARGEPGPTGLP 478 121 GPPGERGGPGSRGFPGADGVAGPKGPAGERGSPGPAGPKGSPGEAGRPGEAGLPGAKGLT 180 GSPGSPGPDGKTGPPGPAGEDGRPGPPGPRGARGEAGVMGFPGPKGAAGEPGKAGERGVP 240 GPPGAVGPAGKDGEAGAEGPPGPAGPAGERGEEGPAGSPGFEGLPGPAGPPGEAGKPGEE 300 GPPGAVGPAGKDGEAGAQGPPGPAGPAGERGEQGPAGSPGFQGLPGPAGPPGEAGKPGEQ 658 GVPGDLGAPGPSGARGEPGFPGERGVEGPPGPAGPPGADGAPGDDGAKGDAGAPGAPGSE 360 GVPGDLGAPGPSGARGERGFPGERGVQGPPGPAGPRGANGAPGNDGAKGDAGAPGAPGSQ 718 1 GSEGPEGVRGEPGPPGPAGAAGPAGDPGADGEPGAKGADGAPGIAGAPGFPGARGPSGPE 60 GSPGSPGFDGKTGPPGPAGQDGRPGPPGPRGQARGQAGVMGFPGPKGAAGEPGKAGERGVP 361 GAPGLEGMPGERGAAGLPGPKGDRGDAGPKGADGSPGKDGVRGLTGPIGPPGPAGAPGDK Gaps 96.6%; Score 2966; DB 5; Length 1461; 95.6%; Pred. No. 3.5e-169; ive 21; Mismatches 3; Indels 0 Indels Best Local Similarity 95.6 Matches 520; Conservative Sequence 1461 AA; 61 181 539 241 599 301 629 Query Match ઠે g à g ò Db g g ò à ò

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GPAGPAGPPGPIGDVGAPGAKGARGSAGPPGATGFPGAAGRVGPPGPSGDAGPPGPA 540 481

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Search completed: September 24, 2004, 11:09:16 Job time : 76.4117 secs

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21, Appl 21, Appl 21, Appl 62, Appl 53, Appl 12, Appl 72, Appl 73, Appl 68, Appl 68, Appl 103, Appl

Sequence Sequence Sequence

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Sequence 103,

ALIGNMENTS

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RESULT 1

US-09-585-887-9

Sequence 9, Application US/09585887

Patent No. 6413742

GENERAL INCORMATION:
APPLICANT: Chang, Robert
APPLICANT: Chang, Robert
APPLICANT: Chang, Robert
APPLICANT: Chang, Robert
APPLICANT: Chisholm, George
TITLE OF INVENTION: NOVEL METHODS FOR THE PRODUCTION OF GELATIN AND
TITLE OF INVENTION: FULL-LENGTH TRIPLE HELICAL COLLAGEN IN RECOMBINANT
TITLE OF INVENTION: CELLS
FILE REFERENCE: 22002030400
CURRENT APPLICATION NUMBER: US/289,578
FRIOR RELING DATE: 1999-04-09
PRIOR FILING DATE: 1999-04-09
PRIOR FILING DATE: 1998-05-08
PRIOR FILING DATE: 1998-05-08

NUMBER OF SEQ ID NOS: 11

SEQ ID NOS: 11

SEQ ID NOS: 12

FIRMATH. 14.4
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US-09-289-578-10
US-08-963-825-21
US-09-550-81-21
US-09-550-81-21
US-09-510-84-4
US-08-642-255-62
US-08-642-255-53
US-08-642-255-53
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US-08-642-255-73
US-08-642-255-73
US-08-119-849-3
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1 GSEGPEGVRGEPGPPGPAGA......PGPSGDAGPPGPPGFAGKEG 544
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                                 GenCore version 5.1.6
(c) 1993 - 2004 Compugen Ltd.
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US-09-331-347C-21

US-09-331-347C-21

Sequence 21, Application US/09331347C

Parent No. 6617431

GENERAL INFORMATION:
APPLICANT: Meristem Therapeutics, S.A.
APPLICANT: Meristem Therapeutics, S.A.
TITLE OF INVENTION: cocmbinant Collagens and Derived Proteins Produced by Plants, Met
TITLE OF INVENTION: obtaining Such and Their Uses
TITLE OF INVENTION: obtaining Such and Their Uses
CURRENT APPLICATION NUMBER: US/09/331,347C

CURRENT FILING DATE: 1999-08-17

NUMBER OF SEQ ID NOS: 22

SOUTWARE: Patentin Version 3.1

SEQ ID NO 21
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                                                                                                           GAPGLQGMPGERGAAGLPGPKGDRGDAGPKGADGSPGKDGVRGLTGP1GPPGPAGAPGDK
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301 GVPGDLGAPGPSGARGEPGFPGERGVEGPPGPAGPPGADGAPGDDGAKGDAGAPGSE
                       361 GAPGLEGMPGERGAAGLPGPKGDRGDAGPKGADGSPGKDGVRGLTGPIGPPGPAGAPGDK
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Best Local Similarity 95.6%; Pred. No. 8.9e-177;
Matches 520; Conservative 21; Mismatches 3; Indels 0
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US-09-331-347C-21
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APPLICANT: Olsen, David R
APPLICANT: Chang, Robert
APPLICANT: Chang, Robert
APPLICANT: Chang, Robert
APPLICANT: Chang, Robert
APPLICANT: Chisholm, George
TITLE OF INVENTION: NOVEL METHODS FOR THE PRODUCTION OF GELATIN AND
TITLE OF INVENTION: FULL-LENGTH TRIPLE HELICAL COLLAGEN IN RECOMBINANT
TITLE OF INVENTION: CULL.
FILE REFERENCE: 225002030400
CURRENT APPLICATION NUMBER: US/09/289,578
CURRENT APPLICATION NUMBER: 60/084,828
PRIOR FILING DATE: 1999-04-10
PRIOR FILING DATE: 1998-05-08
NUMBER OF SEQ ID NOS: 11
SOFTWARE: PATENTIN VOS: 1.
SEQ ID NO 9
SEQ ID NOS: 11
TYPE: PRT
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                                                                                 GVPGDLGAPGPSGARGERGFPGERGVQGPPGPAGPRGANGAPGNDGAKGDAGAPGAPGSQ 718
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  599 GPPGAVGPAGKDGEAGAQGPPGPAGPAGERGEQGPAGSPGFQGLPGPAGPPGEAGKPGEQ 658
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96.6%; Score 2966; DB 4;

Best Local Similarity 95.6%; Pred. No. 8.9e-177;

Matches 520; Conservative 21; Mismatches 3;
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Patent No. 6428978
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US-09-289-578-9
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   543 GAPGLQGMPGERGAAGLPGPKGDRGDAGPKGADGSPGKDGARGLTGP1GPPGPAGAPGDK 602
                                                                                                                261 GPGGPTGARGLVGEPGPAGSKGESGNKGEPGSAGPQGPPGPSGEEGKRGPNGEAGSAGPP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 1, Application US/08931820
| Patent No. 6010863
| GENERAL INFORMATION:
| APPLICANT:
| TITLE OF INVENTION: Assay for collagen degradation NUMBER OF SEQUENCES: 4 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: BE PC COMPATIBLE OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO) CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/931,820
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CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 96202596.1
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R: US/08/931,820
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INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1057 amino acids
TYPE: amino acid
STRANDEDNESS: single
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MOLECULE TYPE: protein
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
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US-08-931-820-1
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APPLICANT: VAN HERENDE, JENS C.
APPLICANT: VAN HERENDE, JENS C.
APPLICANT: DE WOLF, FREDERIK A.
APPLICANT: DE WOLF, FREDERIK A.
APPLICANT: MCOBROEK, ANDREAS
APPLICANT: WERTEN WARC W.T.
APPLICANT: WIND, RICHELE D.
APPLICANT: WIND, RICHELE D.
APPLICANT: VAN DEN BOSCH, TANJA J.
TITLE OF INVENTION: SUITABLE FOR PHOTOGRAPHIC APPLICATION AND ALSO THE TITLE OF INVENTION: PREPARATION THEREOF
TITLE OF INVENTION: SUITABLE FOR PHOTOGRAPHIC APPLICATION AND ALSO THE FILE REFREENCE: 2728-2
CURRENT APPLICATION NUMBER: US/09/219,849
CURRENT FILING DATE: 1998-12-23
NUMBER OF SEQ ID NOS: 50
SOFTWARE: PARCENT NEXT OF SEQ ID NOS: 50
SOFTWARE NEXT OF SEQ ID NOS: 50

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   480
                                              782 GESGPSGPAGPTGARGAPGDRGEPGPPGPPGFAGPPGADGQPGAKGEPGDAGAKGDAGPP 841
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421 GESGPSGPAGPTGARGAPGDRGEPGPPGPAGPPGADGEPGAKGEPGDAGAKGDAGPP
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93.1%; Score 2857; DB 3; Length 822;
Best Local Similarity 91.4%; Pred. No. 3.1e-170;
Matches 497; Conservative 28; Mismatches 19; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; Sequence 49, Application US/09219849 ; Patent No. 6150081
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                     541 GKEG 544
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|GKEG 905
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GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 4
US-09-219-849-49
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A Method for Assaying Collagen Fragments

In Body Fluids, A Test Kit and Means for Carrying Out the Method and Use of the Method to Diagnose the Presence of Disorders Associated with the Metabolism of
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                                                                                                                       211 GASGPMGPRGPPGPPGKBGBBGZAGKPGRPGZRGPPGPZGARGLPGTAGLPGMKGHRGFS
                                                                                                                                                                                                                                                                                                              451 GOAGVMGFPGPKGAAGEPGKAGERGVPGPPGAVGPAGKDGEAGAQGPPGPAGPAGERGEQ
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                                                                                                                                                                              -----GPSGPEG-----PG--GPPGPKGDSGEPGAPGSKGDTGAKGEPGPV
                                                                                                                                                                                                                            271 GLBGAKGBAĞPAĞPKĞZPGSPGZBGAPĞZMĞPPĞPKĞNSĞEPGAPGSKGDTGAKGEPGPV
                                                                                                                                                                                                                                                                                   GVEGPPGPPGPECKPGARGEPGPTGLPGPPGERGGPGSRGFPGADGVAGPKGPAGERGSP
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                                                                      1 GSEGPEGVRGEPGPPGPAGAAGPAGDPGADGE---PGAKGADGAPGIAGAPGFPGAR---
                        Gaps
                     27;
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SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/500,811
FILING DATE: CLASSIFICATION:
PRIOR APPLICATION DATA:
                           23;
Pred. No. 5.5e-166;
; Mismatches 23;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 18, Application US/09500811
| Patent No. 632314
| APPLICANT: QVIET, Per APPLICANT: QVIET, Per APPLICANT: QVIET, Per TITLE OF INVENTION: Method for As TITLE OF INVENTION: Method and Use TITLE OF INVENTION: Disorders Associated the Country No. 100 and No. 10
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
  Similarity
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US-09-500-811-18
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of
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                                                                                                                                GAPGLQCMPGERCAAGLPCPKGDAGPKCAAGSPCKDGVRGLTGPIGPPGPACAPGDK 620
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                                GESGPSGPAGPTGARGAPGDRGEPGPPGPAGFAGPPGADGQPGAKGEPGDAGAKGDAGPP
                                                                                                                                                                                                                                                                                                              GPAGPAGPPGPIGDVGAPGAKGARGSAGPPGATGFPGAAGRVGPPGPSGDAGPPGPPAPA
                                                                                                    GAPGLEGMPGERGAAGLPGPKGDRGDAGPKGADGSPGKDGVRGLTGPIGPPGPAGAPGDK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION: 436
PRIOR APPLICATION DATA:
APPLICATION UNDER: US/08/187,319
FILING DATE: 21-JAN-1994
ATTORNEY/AGENT INFORMATION:
NAWE: GOGOTIS, Adda C
REGISTRATION NUMBER: 29,714
REFERENCE/DOCKET NUMBER: 4305/08701
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US/08/963,825
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          : Floppy disk
IBM PC compatible
YSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 18, Application US/08963825
Patent No. 6110689
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COLLAGEN ALPHA 1 (I)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: A Method TITLE OF INVENTION: in Body ITILE OF INVENTION: in Body ITILE OF INVENTION: in Body ITILE OF INVENTION: Disorder NUMBER OF SEQUENCES: 21 CORRESPONDENCE ADDRESS: ADDRESSEE: Darby & Darby FOREST: 805 Third Avenue CITY: New York STATE: New York COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        : 1341 amino acids
amino acid
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212-753-6237
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APPLICANT: Bonde, Martin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEX: 236687
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ZIP: 10022
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                GKEG 544
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TELEFAX: 21
TELEX: 2366
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US-08-963-825-18
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TYPE: am
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TITLE OF INVENTION: A Method for Assaying Collagen Fragments
TITLE OF INVENTION: in Body Fluids, A Test Kit and Means for Carrying Out
TITLE OF INVENTION: Method and Use of the Method to Diagnose the Presence
TITLE OF INVENTION: Disorders Associated with the Metabolism of
CORRESPONDENCES: 21
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REGISTRATION NUMBER: 29,714
REPERENCE/POCKET VIMBER: 4305/08701
TELEPHONE: 212-527-7700
TELEPHONE: 212-527-7700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/187,319
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IMMEDIATE SOURCE:
CLONE: COLLAGEN ALPHA 1 (I)
                                                                                                                                                                                               Darby & Darby
                                                                                                                                                                                                                       805 Third Avenue
New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     : 1341 amino acids
amino acid
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: protein ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          linear
                                                                                                                                                                                                                                                                                     New York
                                                                                                                                                                                                                                                                                                            USA
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STREET: 805
CITY: New Y
STATE: New
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 1341;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                90.9%; Score 2791.5; DB 4
87.6%; Pred. No. 5.5e-166;
ive 21; Mismatches 23;
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APPLACEMENT INFORMATION:
RILING DATE:
NAME: GOGOTIS, Adda C
REGISTRATION NUMBER: 29,714
REGISTRATION NUMBER: 4305/08701
TELECOMMUNICATION INFORMATION:
TELEFAN: 212-527-7700
TELEFAN: 212-53-6237
TELEFA: 236687
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 1341 amino acids
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IMMEDIATE SOURCE:
CLONE: COLLAGEN ALPHA 1 (I)
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MOLECULE TYPE: protein
ORIGINAL SOURCE:
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Matches 500; Conserv
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US-09~500-811-18
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                                                                                                                                                                                                                                                                                                                             154 GPAGPKGSPGEAGRPGEAGLPGAKGLTGSPGSPGPDGKTGPPGPAGEDGRPGPPGPPGAR
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                                                                                                                                                                                               55 -----GPSGPEG----PG--GPPGPKGDSGEPGAPGSKGDTGAKGEPGPV
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                                                27; Gaps
                                                                                              1 GSEGPEGVRGEPGPPGPAGAAGPAGDPGADGE---PGAKGADGAPGIAGAPGFPGAR-
     DB 4; Length 1341;
Query Match
90.9%; Score 2791.5; DB 4; Length
Best Local Similarity 87.6%; Pred. No. 5.5e-166;
Matches 500; Conservative 21; Mismatches 23; Indels
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Sequence 18, Application US/09570573 Patent No. 6342361 GENERAL INFORMATION: APPLICANT: QVist, Per

US-09-570-573-18

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GFPGAAGRVGPPGPSGDAGPPGPPGPAGKEG 544
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   GPPGADGAPGDDGAKGDAGAPGAPGSEGAPGLEGMPGERGAAGLPGPKGDRGDAGPKGAD 393
                      GSPGKDGVRGLTGPIGPPGPAGAPGDKGESGPSGPAGPTGARGAPGDRGEPGPPGPAGFA
                                                                                                                         GPPGADGEPGAKGEPGDAGAKGDAGPPGPAGPAGPPGPIGDVGAPGAKGARGSAGPPGAT
                                                                                                                                                      691 GPPGADGOPGAKGEPGDAGAKGDAGPPGPAGPPGPIGNVGAPGAKGARGSAGPPGAT
                                                             GSPGKDGVRGLTGPIGPPGPAGAPGDKGESGPSGPAGPTGARGAPGDRGEPGPPGPAGFA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDIUM TYPE: Floppy disk COMPUTER: IBM PC Compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, Version #1.25 APPLICATION DATA: US/09/548,608 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               23;
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90.9%; Score 2791.5; DB 4
Best Local Similarity 87.6%; Pred. No. 5.5e-166;
Matches 500; Conservative 21; Mismatches 23;
                                                                                                                                                                                                   514 GFPGAAGRVGPPGPSGDAGPPGPPGFAGKEG 544
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PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
PFILING DATE:
ATTORNEY/AGENT INFORMATION:
MAME: GOGOTIS, Adda C.
REGISTRATION NUMBER: 29,714
REFERENCE/DOCKET NUMBER: 4305/08701
TELECOMMULICATION INFORMATION:
TELEFROM: 212-527-7700
TELEFRX: 212-5237-7700
                                                                                                                                                                                                                                                                           5-09-548-608-18
Sequence 18, Application US/09548608
Patent No. 6355442
                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
APPLICANT: Oviet, Per
APPLICANT: Oviet, Per
APPLICANT: Oviet, Per
TITLE OF INVENTION: in Body Flui
TITLE OF INVENTION: in Body Flui
TITLE OF INVENTION: Disorders AS
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: Darby & Darby PC
STREET: 805 Third Avenue
CITY: New York
STATE: New York
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: 212-753-6237
TELEX: 236687
INFERMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: protein ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ZIP: 10022
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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1 GSEGPEGVRGEPGPPGPAGAAGPAGDPGADGE----PGAKGADGAPGIAGAPGFPGAR---

OS-US-108-10. Application US/08468996

Factor. No. 6645504

GENERAL INFORMATION:

FAPLICANT: MILEY, Ariel

APPLICANT: Almed, Al-Sabbagh

TITLE OF INVENTION: GLOGGOO

FILE OF INVENTION: DYSTANDER SUPPRESSION OF TYPE 1 DIABETES BY ORAL ADMINISTRATION OF

FILE RFFERENCE: 1010/1695-US3

CURRENT APPLICANTON NUMBER: US/08/468,996

CURRENT APPLICATION NUMBER: US/07/469,852

FRIOR PLING DATE: 1990-02-20

FRIOR APPLICATION NUMBER: US 07/460,852

FRIOR APPLICATION NUMBER: US 07/565,334

FRIOR FILING DATE: 1990-01-15

FRIOR FILING DATE: 1990-01-16

FRIOR FILING DATE: 1990-01-16

FRIOR FILING DATE: 1990-01-16

FRIOR FILING DATE: 1990-01-14

FRIOR FILING DATE: 1990-01-14 450 330 390 273 630 690 GVEGPPGPAGEEGKPGARGEPGPTGLPGPPGERGGPGSRGFPGADGVAGPKGPAGERGSP 153 GPAGSPGFEGLPGPAGPPGEAGKPGEEGVPGDLGAPGPSGARGEPGFPGERGVEGPPGPA 333 GPPGADGAPGDDGAKGDAGAPGAPGSEGAPGLEGMPGERGAAGLPGPKGDRGDAGPKGAD 393 391 GPAGPKGSPGEAGRPGEAGLPGAKGLTGSPGSPGPDGKTGPPGPAGQDGRPGPPGPRGAR GEAGVMGFPGPKGAAGEPGKAGERGVPGPPGAVGPAGKDGEAGAEGPPGPAGPAGERGEE GPAGSPGFQGLPGPAGPPGEPGEAGKPGEQGVPGDLGAPGPSGARGERGFPGERGVQGPPGPA 571 GPRGANGAPGNDGAKGDAGAPGAQGAPGLQGMPGERGAAGLPGPKGDRGDAGPKGAD GPPGADGQPGAKGEPGDAGAKGDAGPPGPAGPAGPPGPIGNVGAPGAKGARGSAGPPGAT 331 GVQGPPGPAGEEGKRGARGEPGPTGLPGPPGERGGPGSRGFPGADGVAGPKGPAGERGSP GPPGADGEPGAKGEPGDAGAKGDAGPPGPAGPAGPPGPIGDVGAPGAKGARGSAGPPGAT -----GPSGPEG----PG---PG--GPPGPKGDSGEPGAPGSKGDTGAKGEPGPV GPAGPKGSPGEAGRPGEAGLPGAKGLTGSPGSPGPDGKTGPPGPAGEDGRPGPPGAR GSPGKDGVRGLTGPIGPPGPAGAPGDKGESGPSGPAGPTGARGAPGDRGEPGPPGPAGFA

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GVPGDLGAPGPSGARGEPGFPGERGVEGPPGPAGPPGADGAPGDDGAKGDAGAPGSE 360
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                                                                                                                                                                                                                                                           0; Gaps
                                                                                                                                                                                                                             Length 1060
                                                                                                                                                                                                                            71.7%; Score 2202; DB 3; Length 1
71.9%; Pred. No. 1.7e-129;
ive 40; Mismatches 113; Indels
                                                                                                                                                           ORGANISM: Homo sapiens
TISSUE TYPE: Collagen type II
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 FILING DATE:
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1060 amino acids
                                                                                                                                                                                                                                                             Matches 391; Conservative
                                                                                                             MOLECULE TYPE: protein
HYPOTHETICAL: NO
ORIGINAL SOURCE:
                                                                                 single
                                                              TYPE: amino acid
STRANDEDNESS: sir
TOPOLOGY: linear
                                                                                                 linear
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US-08-963-825-20
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                                                                                                                                                                                                                                             GPEGAQGPRGEPGTPGSPGPAGASGNPGTDGIPGAKGSAGAPGIAGAPGFPGPRGPPDPQ
                                                                                                                                                                                                                                                                                                      GATGPLGPKGQTGKRGIAGFKGEQGPKGEPGPAGPQGAPGPAGEEGKRGARGEPGKGPI
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                                                                                                                                                 Length 1017;
                                                                                                                                                                                Indels.
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                                                                                                                                               72.5%; Score 2226; DB 4; 72.6%; Pred. No. 5.2e-131; iive 39; Mismatches 110;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT:
TITLE OF INVENTION: Assay for collagnumber OF SEQUENCES: 4
COMPUTER READABLE FORM:
MEDIUM TYPE: FLORPY disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EP 96202596.1
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PRIOR FILING DATE: 1990-10-10
NUMBER OF SEQ ID NOS: 13
SOFTWARE: Patentin version 3.1
SEQ ID NO 10
                                                                                                                                              Ouery Match
Best Local Similarity 72.69
Matches 395; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: Patentin
CURRENT APPLICATION DA
APPLICATION NUMBER:
                                                                                 TYPE: PRT
CRGANISM: Homo sapiens
US-08-468-996-10
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                                                                 LENGTH: 1017
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US-08-931-820-3
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of
Sequence 20, Application US/08963825;
Sequence 20, Application US/08963825;
Patent No. 6110689;
GENERAL INFORMATION:
APPLICANT: QVist, Per
APPLICANT: Bonde, Martin
TITLE OF INVENTION: A Method for Assaying Collagen Fragments
TITLE OF INVENTION: in Body Fluids, A Test Kit and Means for Carrying Out t
TITLE OF INVENTION: Method and Use of the Method to Diagnose the Presence of
TITLE OF INVENTION: Disorders Associated with the Metabolism of
CORRESPONDENCES: 21
CORRESPONDENCE ADDRESS:
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481 GPAGPAGPPGFIGDVGAPGAKGARGSAGPPGATGFPGAAGRVGPPGPSGDAGPPGPPG 540
                                                      995 GPQGPSGAPGPQGPTGVTGPKGARGAQGPPGATGFPGAAGRVGPPGSNGNPGPPGPPGPS
                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INCRMATION:
APPLICANT: Poole, Anthony R.
APPLICANT: Hollander, Anthony R.
APPLICANT: Hollandurst, R. C.
TITLE OF INVENTION: INMUNOASSAYS FOR THE MEASUREMENT OF
TITLE OF INVENTION: COLLAGEN DENATURATION AND CLEAVAGE IN CARTILAGE
NUMBER OF SEQUENCE: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Mashington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 1418;
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COUNTRY D.S.

ZIP: 20007-5109

COMPUTER READBLE FORM:

MEDIUW TYPE: Floppy disk

COMPUTER: IBM PC compatible

COMPUTER: IBM PC compatible

COMPATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/010,999

FLING DATE: 22-JAN-1998

CLASSIFICATION DATA:

APPLICATION NUMBER: US 08/448,501

FLING DATE: 17-JUL-1995

RION APPLICATION DATA:

APPLICATION NUMBER: US 07/984,123

FLING DATE: 04-DEC-1992

ATTORNEY/AGENT INFORMATION:

NAME: BEACL, Stephen A:

REGISTRATION NUMBER: 29,768

REGISTRATION NUMBER: 29,768
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              71.7%; Score 2202; DB 3; 171.9%; Pred. No. 2.1e-129; ive 40; Mismatches 113;
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                                                                                                                                                                                                                                                                                                                              US-09-010-999-1
; Sequence 1, Application US/09010999
; Patent No. 6132976
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INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1418 amino acids
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Best Local Similarity 71.9%;
Matches 391; Conservative 4
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(202) 672-5399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CITY: Washington STATE: D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: amino acid STRANDEDNESS:
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                                                                                                                                                                                                                       SOFTWARE: PACTON Release #1.0, Version #1.25 CURENT APPLICATION DATA: APPLICATION DATA: APPLICATION NUMBER: US/08/963,825
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71.7%; Score 2202; DB 3; 1
Best Local Similarity 71.9%; Pred. No. 2.1e-129;
Matches 391; Conservative 40; Mismatches 113;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: GOGOTIS, Adda C
REGISTRATION NUMBER: 29,714
REPERENCE/DOCKET NUMBER: 4305/08701
TELECOMUNICATION INFORMATION:
TELEFAX: 212-527-7700
TELEFAX: 212-753-6237
TELEFAX: 236697
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 1418 maino acids
                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION: 436
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/187,319
FILING DATE: 21-QAN-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IMMEDIATE SOURCE:
CLONE: COLLAGEN -ALPHA 1 (II)
                                                                                                                                                      COMPUTER: Floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-normal SPETMARE: PATTERN PREVENT PATTERN PATTER
II: 805 Third Avenue
New York
I: New York
RY: USA
                                                                    USA

LIP: 10022

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppov A'

COMPUTER: IRM
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GY: linear
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Sequence 20, Application US/09570573

Sequence 20, Application US/09570573

Patent No. 6342361

GENERAL INFORMATION:
APPLICANT: Qvist, Per
APPLICANT: Qvist, Per
TITLE OF INVENTION: A Method for Assaying Collagen Fragments
TITLE OF INVENTION: in Body Fluids, A Test Kit and Means for Carrying Out ITLE OF INVENTION: in Body Fluids, A Test Kit and Means for Carrying Out ITLE OF INVENTION: Disorders Associated with the Metabolism of NUMBER OF SEQUENCES: 21

CORRESPONDENCE ADDRESS:
ADDRESSEB: Darby & Darby PC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                420
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                                                                                                                                                                                                           Length 1418;
                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                              71.7%; Score 2202; DB 4;
71.9%; Pred. No. 2.1e-129;
iive 40; Mismatches 113;
              | LENGTH: 1418 amino acids
| TYPE: amino acid
| TYPE: amino acid
| TYPE: amino acid
| MOLECULE TYPE: protein
| ORIGINAL SOURCE:
| ORGANISM: Homo sapiens
| IMMEDIATE SOURCE:
| CLONE: COLLAGEN -ALPHA 1 (II)
| US-09-500-811-20
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New York
                                                                                                                                                                                                                Query Match
Best Local Similarity 71.9
Matches 391; Conservative
SEQUENCE CHARACTERISTICS LENGTH: 1418 amino ac:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           541 GKEG 544
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855 GKDG 858
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of
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APPLICANT: Qvist, Per

APPLICANT: Qvist, Per

APPLICANT: Bonde, Martin

TITLE OF INVENTION: A Method for Assaying Collagen Fragments

TITLE OF INVENTION: In Body Fluids, A Test Kit and Means for Carrying Out

TITLE OF INVENTION: Method and Use of the Method to Diagnose the Presence

TITLE OF INVENTION: Disorders Associated with the Metabolism of

CORRESPONDENCES: 21

CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           540
                                                                               240
                                                                                                                                                                                                                                                                                                                 GAPGLEGMPGERGAAGLPGPKGDRGDAGPKGADGSPGKDGVRGLTGPIGPPGPAGAPGDK 420
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    GPPGERGGPGSRGFPGADGVAGPKGPAGERGSPGPAGPKGSPGEAGRPGEAGLPGAKGLT 180
                                       494
                                                                                                                                                         GPPGAVGPAGKDGEAGAEGPPGPAGPAGERGEEGPAGSPGFEGLPGPAGPPGEAGKPGEE 300
                                                                                                                                                                                             GAPGLRGLPGKDGETGAEGPPGPAGPAGERGEQGAPGPSGFQGLPGPPGPPGEGGKPGDQ 614
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                      GSPGSPGPDGKTGPPGPAGEDGRPGPPGPRGARGEAGVMGFPGPKGAAGEPGKAGERGVP
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ZIP: 10022
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4305/08701
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APPLICATION NUMBER: 08/187,319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5.09-500-811-20
Sequence 20, Application US/09500811
Patent No. 6323314
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Gogoris, Adda C
REGISTRATION NUMBER: 29,714
REFERENCE/DOCKET NUMBER: 43
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-527-7700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     20:
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         212-753-6237
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ZIE: 10022
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: 1 BM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
FILING DATE:
                                                                                                                                                                   CLASSIFICATION:
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
PILING DATE:
ATORNEY/AGENT INFORMATION:
NAME: GGGOTIS, Adda C
REGISTRATION NUMBER: 29,714
REFERENCE/DOCKET NUMBER: 29,714
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
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TELERAX: 212-75-6237
TELESX: 236687
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHRACTERISTICS:
LENGTH: 1418 amino acids
TYPE: amino acid
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
ORIGINAL SOURCE:
ORGANISM: Home sapiens
IMMEDIATE SOURCE:
COLLAGEN -ALPHA 1 (II)
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Search completed: September 24, 2004, 11:09:50 Job time : 23.3958 secs
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